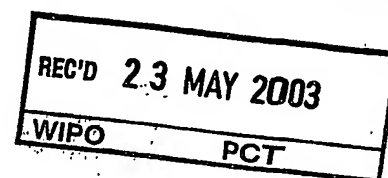


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PATENT- OG VAREMÆRKESTYRELSEN

10 APR. 2002

TITLE: Improved *Bacillus* Host Cell

Modtaget

TECHNICAL FIELD

Bacillus sp. are attractive hosts for the production of heterologous proteins due their ability to secrete proteins directly into the culture medium. They have a high capacity for protein secretion, are genetically highly amenable, nonpathogenic and free of endotoxins, and consequently a large variety of proteins from different organisms have been efficiently produced and secreted in *Bacillus* sp. i.e. in *Bacillus licheniformis*.

Improved *Bacillus* host cells that provide better production economy, or better products e.g. in terms of stability, purity etc. are constantly in demand in the industry.

BACKGROUND

Industrial production in *Bacillus* sp. of products of interest such as heterologous polypeptides, amino acids, carbohydrates etc., even when such a product is secreted into the medium, very often requires a costly purification step of the product from the culture medium. Contaminant polypeptides native to the *Bacillus* production host cell are secreted into the culture medium, and they may have to be removed e.g. in order to ensure the stability of the product, or to obtain a sufficient purity of the product. Typically, the native secreted contaminant polypeptides could be proteolytic enzymes, nutrient uptake factors, signal molecules etc.

Naturally, it is of considerable interest to the industrial producers to reduce the costs associated with product purification steps, indeed it would be of commercial value if one or more purification steps could be completely eliminated.

SUMMARY

A problem to be solved by the present invention is how to reduce the necessary product purification required when producing products of interest in a *Bacillus licheniformis* host cell. The present invention provides a solution to the problem by reducing the amount of contaminant secreted native polypeptide(s) in the culture medium, this is achieved by reducing the expression of such polypeptide(s) in a mutated host cell. Production in a mutant host cell of the invention provides a culture medium with far fewer contaminants, and this in turn makes it much easier to purify the product of interest from the culture medium to the point where certain previously required steps may be completely eliminated from the production process. Production in a mutant host cell of the invention may also have a positive effect on the total product yield and shelf-life, since product stability is often hampered by the presence of contaminant polypeptides in the culture medium.

Accordingly, in a first aspect the invention relates to a *Bacillus licheniformis* mutant host cell derived from a parent *B. licheniformis* host cell, which mutant host cell is mutated in one or more gene(s) encoding one or more secreted polypeptide(s) which is at least 80% identical to one or more of the polypeptides shown in SEQ ID NO's: 2 to 200, preferably at least 85% identical, more preferably at least 90% identical, still more preferably at least 95% identical, and most preferably at least 97% identical to one or more of the polypeptides shown in SEQ ID NO's: 2 to 200, wherein the mutant host cell secretes at least 5% less of the one or more secreted polypeptide(s) than the parent host cell, when they are cultivated under comparable conditions.

Preferably wherein the mutant host cell secretes at least 10% less, more preferably at least 20% less, still more preferably at least 30% less, even more preferably at least 40% less, yet more preferably at least 50% less, or at least 60% less, or at least 70% less, or at least 80%, or most preferably at least 90% less of the one or more secreted polypeptide(s) than the parent host cell, when they are cultivated under comparable conditions. Most preferably the mutant host cell secretes absolutely nothing of the one or more secreted polypeptide(s).

Comparable conditions of cultivation must be used in order to compare the secretion level of one or more secreted polypeptides in a mutant host cell of the invention with that in a parent host cell. They are cultivated separately under identical conditions in identical setups, of course allowing for the usual standard deviations of the operating parameters normally associated with growth experiments, such as temperature control etc. The quantification of the expression level of one or more secreted polypeptide(s) is done by standard text-book assay techniques as known in the art, often based on the biological activity of the one or more secreted polypeptide(s) *i.e.* if a secreted polypeptide is an amylase, then an amylase-activity based quantification assay is used. To quantify a secreted polypeptide of unknown activity, immuno based or mass-spec based assays may be used.

In a second aspect the invention relates to a process for producing at least one product of interest in a *Bacillus licheniformis* mutant host cell, comprising cultivating a *B.licheniformis* mutant host cell as defined in the previous aspect in a suitable medium, whereby the said product is produced.

Finally, an aspect of the invention relates to a use of a *Bacillus licheniformis* mutant host cell as defined in the first aspect for producing at least one product of interest comprising cultivating the mutant host cell in a suitable medium whereby the said product is produced.

DEFINITIONS

Nucleic acid construct: When used herein, the term "nucleic acid construct" means a nucleic acid molecule, either single- or double-stranded, which is isolated from a naturally occurring gene or which has been modified to contain segments of nucleic acids in a manner that would not otherwise exist in nature. The term nucleic acid construct is synonymous with the term "expression cassette" when the nucleic acid construct contains the control sequences required for expression of a coding sequence of the present invention.

Control sequence: The term "control sequences" is defined herein to include all components, which are necessary or advantageous for the expression of a polypeptide of the present invention. Each control sequence may be native or foreign to the nucleotide sequence encoding the polypeptide. Such control sequences include, but are not limited to, a leader, polyadenylation sequence, propeptide sequence, promoter, signal peptide sequence, and transcription terminator. At a minimum, the control sequences include a promoter, and transcriptional and translational stop signals. The control sequences may be provided with linkers for the purpose of introducing specific restriction sites facilitating ligation of the control sequences with the coding region of the nucleotide sequence encoding a polypeptide.

Operably linked: The term "operably linked" is defined herein as a configuration in which a control sequence is appropriately placed at a position relative to the coding sequence of the DNA sequence such that the control sequence directs the expression of a polypeptide.

Coding sequence: When used herein the term "coding sequence" is intended to cover a nucleotide sequence, which directly specifies the amino acid sequence of its protein product. The boundaries of the coding sequence are generally determined by an open reading frame, which usually begins with the ATG start codon. The coding sequence typically include DNA, cDNA, and recombinant nucleotide sequences.

Expression: In the present context, the term "expression" includes any step involved in the production of the polypeptide including, but not limited to, transcription, post-transcriptional modification, translation, post-translational modification, and secretion.

Expression vector: In the present context, the term "expression vector" covers a DNA molecule, linear or circular, that comprises a segment encoding a polypeptide of the invention, and which is operably linked to additional segments that provide for its transcription.

DETAILED DISCLOSURE

A *Bacillus licheniformis* mutant host cell derived from a parent *B. licheniformis* host cell, which mutant host cell is mutated in one or more gene(s) encoding one or more secreted polypeptide(s) which is at least 80% identical to one or more of the polypeptides shown in SEQ ID NO's: 2 to 200, wherein the mutant host cell secretes at least 5% less of the one or more secreted polypeptide(s) than the parent host cell, when they are cultivated under comparable conditions.

The term "parent host cell" in the context of the present invention means a cell which is genetically identical, or isogenic, to the progeny mutant or mutant cell of the present invention, except for the mutated one or more gene(s) encoding one or more secreted polypeptide(s) in said mutant.

The degree of identity, or %-identity of polypeptide sequences can suitably be investigated by aligning the sequences using a computer program known in the art, such as "GAP" provided in the GCG program package (Program Manual for the Wisconsin Package, Version 8, August 1994, Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711)(Needleman, S.B. and Wunsch, C.D., (1970), Journal of Molecular Biology, 48, 443-453). Using GAP with the following settings for DNA sequence comparison: GAP creation penalty of 5.0 and GAP extension penalty of 0.3".

The object of the present invention is to provide a cleaner culture medium so as to reduce the product purification to a minimum, and this may be done according to the invention by reducing or even completely abolishing the expression of genes expressing native secreted polypeptides via mutagenisation of those genes. One of the very well-known method of ensuring that a gene is not expressed into an active polypeptide within a cell is simply to delete or partially delete the encoding gene. Many techniques have been described in the art on how to specifically delete or partially delete one or more gene(s) in the genome of a cell, and certainly from the genome of a *Bacillus licheniformis* cell (see e.g. Novozymes A/S WO 01/90393, Novozymes A/S WO 02/00907, and Example 1 herein). Accordingly, a preferred embodiment of the present invention relates to a host cell of the first aspect, which is mutated by a partial or complete deletion of the one or more gene(s) encoding the one or more secreted polypeptide(s).

A specific example of such a deletion or partial deletion is shown in an example herein, where a gene encoding the native secreted polypeptide shown in SEQ ID NO: 134 is deleted from a *Bacillus licheniformis* host cell. So, a preferred embodiment of the present invention

relates to a host cell of the first aspect, which is mutated by a partial or complete deletion of a gene encoding a secreted polypeptide which is at least 80% identical to the polypeptide shown in SEQ ID NO: 134, more preferably at least 85%, still more preferably at least 90%, even more preferably at least 95%, and most preferably at least 97% identical to the polypeptide shown in SEQ ID NO: 134.

As already mentioned, it is an object of the invention to provide a cleaner culture medium, and the more secreted contaminant polypeptides that are eliminated, the fewer will have to be removed in a subsequent product purification. A preferred embodiment of the present invention relates to a host cell of the first aspect, which is mutated in two or more genes encoding two or more secreted polypeptides.

The product of interest to be produced by the mutant host cell of the first aspect may be one or more polypeptide(s) encoded by one or more heterologous gene(s). Consequently, a preferred embodiment of the present invention relates to a host cell of the first aspect, which comprises one or more heterologous gene(s) encoding one or more heterologous polypeptide(s).

In the industrial production of polypeptides it is of interest to achieve a product yield as high as possible. One way to increase the yield is to increase the copy number of a gene encoding a polypeptide of interest. This can be done by placing the gene on a high copy number plasmid. However, plasmids are unstable and are often lost from the host cells if there is no selective pressure during the cultivation of the host cells. Another way to increase the copy number of the gene of interest is to integrate it into the host cell chromosome in multiple copies. Integration of two genes has been described in WO 91/09129 and WO 94/14968 (Novozymes A/S) the content of which is hereby incorporated by reference. A preferred embodiment of the present invention relates to a host cell of the first aspect, wherein the heterologous gene(s) is present in at least two copies, preferably at least 4 copies, and most preferably at least 6 copies. In another embodiment the heterologous gene(s) is present in at least ten copies. If carried on a plasmid the gene(s) may be present in several hundred copies per cell, so in a still further embodiment of the present invention the heterologous gene(s) is present in at least 100 copies.

Integration of two genes closely spaced in anti-parallel tandem to achieve better stability has been described in WO 99/41358 (Novozymes A/S) the content of which is hereby incorporated by reference, as well as the stable chromosomal multi-copy integration of genes described in WO 02/00907 (Novozymes A/S) the content of which is incorporated herein by

reference. A preferred embodiment of the present invention relates to a host cell of the first aspect, wherein the heterologous gene(s) are stably integrated into the genome of the cell.

5 Selection of chromosomal integrant has for convenience resulted in the use of selectable markers such as antibiotic resistance markers. However it is desirable if possible to avoid the use of antibiotic marker genes. WO 01/90393 discloses a method for the integration of a gene in the chromosome of a host cell without leaving antibiotic resistance markers behind in the strain, the content of which is hereby incorporated by reference. A preferred embodiment of the present invention relates to a host cell of the first aspect wherein the heterologous
10 gene(s) is integrated into the genome of the cell without leaving any antibiotic resistance marker genes at the site of integration.

The present invention also relates to nucleic acid constructs comprising a nucleotide sequence encoding a product of interest, which may be operably linked to one or more
15 control sequences that direct the expression of the coding sequence in a suitable host cell under conditions compatible with the control sequences.

A nucleotide sequence encoding a polypeptide of interest may be manipulated in a variety of ways to provide for expression of the polypeptide. Manipulation of the nucleotide sequence prior to its insertion into a vector may be desirable or necessary depending on the expression
20 vector. The techniques for modifying nucleotide sequences utilizing recombinant DNA methods are well known in the art.

Other ways of increasing the product yield would be to increase promoter activity of the
25 specific promoter regulating the expression of a specific gene of interest. Also a more general increase in the activity of several promoters at the same time could lead to an improved product yield. The control sequence may be an appropriate promoter sequence, a nucleotide sequence which is recognized by a host cell for expression of the nucleotide sequence. The promoter sequence contains transcriptional control sequences, which
30 mediate the expression of the polypeptide. The promoter may be any nucleotide sequence which shows transcriptional activity in the host cell of choice including mutant, truncated, and hybrid promoters, and may be obtained from genes encoding extracellular or intracellular polypeptides either homologous or heterologous to the host cell.

35 Examples of suitable promoters for directing the transcription of the nucleic acid constructs of the present invention, especially in a bacterial host cell, are the promoters obtained from the *E. coli* lac operon, *Streptomyces coelicolor* agarase gene (*dagA*), *Bacillus subtilis*

levansucrase gene (sacB), *Bacillus licheniformis* alpha-amylase gene (amyL), *Bacillus stearothermophilus* maltogenic amylase gene (amyM), *Bacillus amyloliquefaciens* alpha-amylase gene (amyQ), *Bacillus licheniformis* penicillinase gene (penP), *Bacillus subtilis* xylA and xylB genes, and prokaryotic beta-lactamase gene (Villa-Kamaroff et al., 1978, 5 Proceedings of the National Academy of Sciences USA 75: 3727-3731), as well as the tac promoter (DeBoer et al., 1983, Proceedings of the National Academy of Sciences USA 80: 21-25). Further promoters are described in "Useful proteins from recombinant bacteria" in Scientific American, 1980, 242: 74-94; and in Sambrook et al., 1989, supra.

10 Other useful promoters are described in WO 93/10249, WO 98/07846, and WO 99/43835 (Novozymes A/S) the contents of which are incorporated fully herein by reference. A preferred embodiment of the present invention relates to a host cell of the first aspect, wherein the heterologous gene(s) are transcribed from a heterologous promoter or from an artificial promoter.

15 The control sequence may also be a suitable transcription terminator sequence, a sequence recognized by a host cell to terminate transcription. The terminator sequence is operably linked to the 3' terminus of the nucleotide sequence encoding the polypeptide. Any terminator which is functional in the host cell of choice may be used in the present invention.

20 The control sequence may also be a suitable leader sequence, a nontranslated region of an mRNA which is important for translation by the host cell. The leader sequence is operably linked to the 5' terminus of the nucleotide sequence encoding the polypeptide. Any leader sequence that is functional in the host cell of choice may be used in the present invention.

25 The control sequence may also be a polyadenylation sequence, a sequence operably linked to the 3' terminus of the nucleotide sequence and which, when transcribed, is recognized by the host cell as a signal to add polyadenosine residues to transcribed mRNA. Any polyadenylation sequence which is functional in the host cell of choice may be used in the 30 present invention.

The control sequence may also be a signal peptide coding region that codes for an amino acid sequence linked to the amino terminus of a polypeptide and directs the encoded polypeptide into the cell's secretory pathway. The 5' end of the coding sequence of the 35 nucleotide sequence may inherently contain a signal peptide coding region naturally linked in translation reading frame with the segment of the coding region which encodes the secreted polypeptide. Alternatively, the 5' end of the coding sequence may contain a signal peptide

coding region which is foreign to the coding sequence. The foreign signal peptide coding region may be required where the coding sequence does not naturally contain a signal peptide coding region. Alternatively, the foreign signal peptide coding region may simply replace the natural signal peptide coding region in order to enhance secretion of the polypeptide. However, any signal peptide coding region which directs the expressed polypeptide into the secretory pathway of a host cell of choice may be used in the present invention.

Effective signal peptide coding regions for bacterial host cells are the signal peptide coding regions obtained from the genes for *Bacillus* NCIB 11837 maltogenic amylase, *Bacillus stearothermophilus* alpha-amylase, *Bacillus licheniformis* subtilisin, *Bacillus licheniformis* beta-lactamase, *Bacillus stearothermophilus* neutral proteases (nprT, nprS, nprM), and *Bacillus subtilis* prsA. Further signal peptides are described by Simonen and Palva, 1993, *Microbiological Reviews* 57: 109-137.

The control sequence may also be a propeptide coding region that codes for an amino acid sequence positioned at the amino terminus of a polypeptide. The resultant polypeptide is known as a proenzyme or propolypeptide (or a zymogen in some cases). A propolypeptide is generally inactive and can be converted to a mature active polypeptide by catalytic or autocatalytic cleavage of the propeptide from the propolypeptide. The propeptide coding region may be obtained from the genes for *Bacillus subtilis* alkaline protease (aprE), *Bacillus subtilis* neutral protease (nprT), *Saccharomyces cerevisiae* alpha-factor, *Rhizomucor miehei* aspartic proteinase, and *Myceliophthora thermophila* laccase (WO 95/33836).

Where both signal peptide and propeptide regions are present at the amino terminus of a polypeptide, the propeptide region is positioned next to the amino terminus of a polypeptide and the signal peptide region is positioned next to the amino terminus of the propeptide region.

It may also be desirable to add regulatory sequences which allow the regulation of the expression of the polypeptide relative to the growth of the host cell. Examples of regulatory systems are those which cause the expression of the gene to be turned on or off in response to a chemical or physical stimulus, including the presence of a regulatory compound. Regulatory systems in prokaryotic systems include the lac, tac, and trp operator systems. In yeast, the ADH2 system or GAL1 system may be used. In eukaryotic systems, these include the dihydrofolate reductase gene which is amplified in the presence of methotrexate, and the

metallothionein genes which are amplified with heavy metals. In these cases, the nucleotide sequence encoding the polypeptide would be operably linked with the regulatory sequence.

5 The present invention also relates to recombinant expression vectors comprising the nucleic acid construct of the invention. The various nucleotide and control sequences described above may be joined together to produce a recombinant expression vector which may include one or more convenient restriction sites to allow for insertion or substitution of the nucleotide sequence encoding the polypeptide at such sites. Alternatively, the nucleotide sequence of the present invention may be expressed by inserting the nucleotide sequence or
10 a nucleic acid construct comprising the sequence into an appropriate vector for expression. In creating the expression vector, the coding sequence is located in the vector so that the coding sequence is operably linked with the appropriate control sequences for expression.

The recombinant expression vector may be any vector (e.g., a plasmid or virus) which can be
15 conveniently subjected to recombinant DNA procedures and can bring about the expression of the nucleotide sequence. The choice of the vector will typically depend on the compatibility of the vector with the host cell into which the vector is to be introduced. The vectors may be linear or closed circular plasmids.

20 The vector may be an autonomously replicating vector, i.e., a vector which exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, e.g., a plasmid, an extrachromosomal element, a minichromosome, or an artificial chromosome.

25 The vector may contain any means for assuring self-replication. Alternatively, the vector may be one which, when introduced into the host cell, is integrated into the genome and replicated together with the chromosome(s) into which it has been integrated. Furthermore, a single vector or plasmid or two or more vectors or plasmids which together contain the total DNA to be introduced into the genome of the host cell, or a transposon may be used.

30

The vectors of the present invention preferably contain one or more selectable markers which permit easy selection of transformed cells. A selectable marker is a gene the product of which provides for biocide or viral resistance, resistance to heavy metals, prototrophy to auxotrophs, and the like.

35

Examples of bacterial selectable markers are the *dal* genes from *Bacillus subtilis* or *Bacillus licheniformis*, or markers which confer antibiotic resistance such as ampicillin, kanamycin, chloramphenicol or tetracycline resistance.

- 5 The vectors of the present invention preferably contain an element(s) that permits stable integration of the vector into the host cell's genome or autonomous replication of the vector in the cell independent of the genome.

10 For integration into the host cell genome, the vector may rely on the nucleotide sequence encoding the polypeptide or any other element of the vector for stable integration of the vector into the genome by homologous or nonhomologous recombination. Alternatively, the vector may contain additional nucleotide sequences for directing integration by homologous recombination into the genome of the host cell. The additional nucleotide sequences enable the vector to be integrated into the host cell genome at a precise location(s) in the
15 chromosome(s). To increase the likelihood of integration at a precise location, the integrational elements should preferably contain a sufficient number of nucleotides, such as 100 to 1,500 base pairs, preferably 400 to 1,500 base pairs, and most preferably 800 to 1,500 base pairs, which are highly homologous with the corresponding target sequence to enhance the probability of homologous recombination. The integrational elements may be
20 any sequence that is homologous with the target sequence in the genome of the host cell. Furthermore, the integrational elements may be non-encoding or encoding nucleotide sequences. On the other hand, the vector may be integrated into the genome of the host cell by non-homologous recombination.

- 25 For autonomous replication, the vector may further comprise an origin of replication enabling the vector to replicate autonomously in the host cell in question. Examples of bacterial origins of replication are the origins of replication of plasmids pBR322, pUC19, pACYC177, and pACYC184 permitting replication in *E. coli*, and pUB110, pE194, pTA1060, and pAMB1 permitting replication in *Bacillus*. The origin of replication may be one having a mutation
30 which makes its functioning temperature-sensitive in the host cell (see, e.g., Ehrlich, 1978, Proceedings of the National Academy of Sciences USA 75: 1433).

35 More than one copy of a nucleotide sequence of the present invention may be inserted into the host cell to increase production of the gene product. An increase in the copy number of the nucleotide sequence can be obtained by integrating at least one additional copy of the sequence into the host cell genome or by including an amplifiable selectable marker gene with the nucleotide sequence where cells containing amplified copies of the selectable

marker gene, and thereby additional copies of the nucleotide sequence, can be selected for by cultivating the cells in the presence of the appropriate selectable agent.

5 The procedures used to ligate the elements described above to construct the recombinant expression vectors of the present invention are well known to one skilled in the art (see, e.g., Sambrook et al., 1989, supra).

10 The introduction of a vector into a bacterial host cell may, for instance, be effected by protoplast transformation (see, e.g., Chang and Cohen, 1979, Molecular General Genetics 168: 111-115), using competent cells (see, e.g., Young and Spizizin, 1961, Journal of Bacteriology 81: 823-829, or Dubnau and Davidoff-Abelson, 1971, Journal of Molecular Biology 56: 209-221), electroporation (see, e.g., Shigekawa and Dower, 1988, Biotechniques 6: 742-751), or conjugation (see, e.g., Koehler and Thorne, 1987, Journal of Bacteriology 169: 5771-5278).

15 A preferred embodiment of the present invention relates to a host cell of the first aspect, wherein the heterologous gene(s) are comprised in an operon, preferably a polycistronic operon. The term "operon" in the context of the present invention means a polynucleotide comprising several genes that are clustered and perhaps even transcribed together into a polycistronic mRNA, e.g. genes coding for the enzymes of a metabolic pathway. The transcription of an operon may be initiated at a promoter region and controlled by a neighboring regulatory gene, which encodes a regulatory protein, which in turn binds to the operator sequence in the operon to respectively inhibit or enhance the transcription. The gene or the operon can be carried on a suitable plasmid that can be stably maintained, e.g. 20 capable of stable autonomous replication in the host cell (the choice of plasmid will typically depend on the compatibility of the plasmid with the host cell into which the plasmid is to be introduced) or it can be carried on the chromosome of the host. The said gene may be endogenous to the host cell in which case the product of interest is a protein naturally produced by the host cell and in most cases the gene will be in its normal position on the chromosome. If the gene encoding the product of interest is an exogenous gene, the gene 30 could either be carried on a suitable plasmid or it could be integrated on the host chromosome. In one embodiment of the invention the eubacterium is a recombinant eubacterium. Also the product of interest may in another embodiment be a recombinant protein.

35 The product of interest is any gene product or product of a metabolic pathway which is industrially useful and which can be produced in a bacterial cell such as a *B. licheniformis*.

In one preferred embodiment, the heterologous polypeptide(s) is an antimicrobial peptide, or a fusion peptide comprising a peptide part which in its native form has antimicrobial activity.

- 5 In another preferred embodiment, the heterologous polypeptide(s) has biosynthetic activity and produces a compound or an intermediate of interest.

Yet another embodiment relates to a host cell of the first aspect, wherein the compound or intermediate of interest comprises vitamins, amino acids, antibiotics, carbohydrates, or
10 surfactants, and preferably the carbohydrates comprise hyaluronic acid.

In one embodiment the heterologous polypeptide(s) is an enzyme, particularly the enzyme is an enzyme of a class selected from the group of enzyme classes consisting of oxidoreductases (EC 1), transferases (EC 2), hydrolases (EC 3), lyases (EC 4), isomerases
15 (EC 5), and ligases (EC 6). Preferably the enzyme is an enzyme with an activity selected from the group consisting of aminopeptidase, amylase, amyloglucosidase, mannanase, carbohydrase, carboxypeptidase, catalase, cellulase, chitinase, cutinase, cyclodextrin glycosyltransferase, deoxyribonuclease, esterase, galactosidase, beta-galactosidase, glucoamylase, glucose oxidase, glucosidase, haloperoxidase, hemicellulase, invertase,
20 isomerase, laccase, ligase, lipase, lyase, mannosidase, oxidase, pectinase, peroxidase, phytase, phenoloxidase, polyphenoloxidase, protease, ribonuclease, transferase, transglutaminase, or xylanase. Preferably the enzyme is an amylase or a mannanase.

A second aspect of the invention relates to a process for producing at least one product of
25 interest in a *Bacillus licheniformis* mutant host cell, comprising cultivating a *B.licheniformis* mutant host cell as defined in the first aspect of the invention in a suitable medium, whereby the said product is produced. One embodiment relates to a process of the second aspect, further comprising isolating or purifying the product of interest. Suitable media for the cultivation is described below as well as methods for the purification or isolation of the
30 produced product which is an optional additional step to the process of the present invention.

In the production methods of the present invention, the cells are cultivated in a nutrient medium suitable for production of the polypeptide using methods known in the art. For example, the cell may be cultivated by shake flask cultivation, small-scale or large-scale
35 fermentation (including continuous, batch, fed-batch, or solid state fermentations) in laboratory or industrial fermentors performed in a suitable medium and under conditions allowing the polypeptide to be expressed and/or isolated. The cultivation takes place in a

suitable nutrient medium comprising carbon and nitrogen sources and inorganic salts, using procedures known in the art. Suitable media are available from commercial suppliers or may be prepared according to published compositions (e.g., in catalogues of the American Type Culture Collection). If the polypeptide is secreted into the nutrient medium, the polypeptide can be recovered directly from the medium. If the polypeptide is not secreted, it can be recovered from cell lysates.

The medium used to culture the cells may be any conventional medium suitable for growing the host cells, such as minimal or complex media containing appropriate supplements. Suitable media are available from commercial suppliers or may be prepared according to published recipes (e.g. in catalogues of the American Type Culture Collection). The media are prepared using procedures known in the art (see, e.g., references for bacteria and yeast; Bennett, J.W. and LaSure, L., editors, *More Gene Manipulations in Fungi*, Academic Press, CA, 1991).

The polypeptides may be detected using methods known in the art that are specific for the polypeptides. These detection methods may include use of specific antibodies, formation of an enzyme product, or disappearance of an enzyme substrate. For example, an enzyme assay may be used to determine the activity of the polypeptide as described herein.

The resulting polypeptide may be recovered by methods known in the art. For example, the polypeptide may be recovered from the nutrient medium by conventional procedures including, but not limited to, centrifugation, filtration, extraction, spray-drying, evaporation, or precipitation.

The polypeptides of the present invention may be purified by a variety of procedures known in the art including, but not limited to, chromatography (e.g., ion exchange, affinity, hydrophobic, chromatofocusing, and size exclusion), electrophoretic procedures (e.g., preparative isoelectric focusing), differential solubility (e.g., ammonium sulfate precipitation), SDS-PAGE, or extraction (see, e.g., *Protein Purification*, J.-C. Janson and Lars Ryden, editors, VCH Publishers, New York, 1989).

A third aspect of the present invention relates to the use of a *Bacillus licheniformis* mutant host cell as defined in the first aspect for producing at least one product of interest comprising cultivating the mutant host cell in a suitable medium whereby the said product is produced, and optionally isolating or purifying the produced product.

The present invention is further illustrated by the following examples, which, however, are not to be construed as limiting the scope of protection. The features disclosed in the foregoing description and in the following examples may, both separately and in any combination thereof, be material for realising the invention in diverse forms thereof.

5

EXAMPLES

Example 1

10 The gene encoding a small extracellular protein from *B. licheniformis* is included in the sequence shown in SEQ ID NO: 133, where the start codon of the protein encoding sequence is the ATG in position 601, and the stopcodon is the TAA in position 979.

A vector designed to allow deletion of the entire open reading frame is constructed as follows:

15

1) An upstream DNA fragment is prepared by PCR amplification using chromosomal *B. licheniformis* DNA as template and the following primers:

EcoRI <L12 574-594> (SEQ ID NO: 201)

20 5'-gactgaattcgtgcgagttcctccacattcg-3'

HindIII BglII<L12 1074-1052> (SEQ ID NO: 202)

5'-gactaagcttagatctactctataagtttagtttgcacc-3'

25 The amplified fragment is digested with EcoRI og HindIII, inserted between the EcoRI and HindIII sites in pUC19, and the ligation mixture transformed into *E. coli* selecting ampicillin resistance (200 microg/ml).

30 2) The cloned DNA fragment is excised as an EcoRI-BglII fragment, and ligated to the 5.1 kb EcoRI-BglII fragment of pSJ2739 (Described in U.S. Patent 6,100,063, Fig. 10). The ligation mixture is transformed into *B. subtilis* DN1885 (Diderichsen et al., 1990 (Diderichsen, B., Wedsted, U., Hedegaard, L., Jensen, B. R., Sjøholm, C. (1990). Cloning of aldB, which encodes α -acetolactate decarboxylase, an exoenzyme from *Bacillus brevis*. J. Bacteriol. 172, 4315-4321)), selecting erythromycin resistance (5 microg/ml) at 30 °C.

35

3) A downstream DNA fragment is prepared by PCR amplification using chromosomal *B. licheniformis* DNA as template and the following primers:

KpnI BglII BamHI<L12 1500-1520> (SEQ ID NO: 203)
5'-gactggtaccagatctggatccgaaaacggttgctgtcaacgg-3'

5 HindIII<L12 2007-1986> (SEQ ID NO: 204)
5'-gactaagcttatcttttgtggagatgctttgg-3'

The amplified fragment is digested with KpnI and HindIII, and inserted into KpnI + HindIII digested pUC19. Transformation is into *E. coli*.

10

4) A DNA fragment containing a spectinomycin resistance gene (*spc*) flanked by resolvase sites (*res*) originating from plasmid pAM β 1 is excised as a 1.5 kb BclI-BamHI fragment from plasmid pSJ3358 (described in U.S. Patent 5,882,888), and inserted into the BamHI site of the plasmid constructed above, under 3). Transformation is into *E. coli*.

15

5) The entire "*res-spc-res*-downstream DNA fragment" segment is excised from the plasmid prepared under 4), above, using enzymes BglII and HindIII, and is inserted in the plasmid prepared under 2), above, which has been digested with BglII and HindIII. Transformation is into *B. subtilis* DN1885, selecting spectinomycin resistance (120 μ g/ml) and erythromycin resistance (5 μ g/ml) at 30 °C.

20

6) The plasmid constructed under 5), above, is transformed into donor strain PP289-5 (described in US 5,882,888) for easy transfer into *B. licheniformis* by conjugation.

25

B. licheniformis strains, which do not produce the small extracellular protein, are constructed by the following procedure:

30 The plasmid constructed under 5), above, is transferred into the *B. licheniformis* strain by conjugation from the *B. subtilis* donor strain constructed under 6), above, as described in US 5,882,888. Strains, in which the plasmid has integrated into the chromosome, are selected by isolation of colonies able to grow at 50 °C on plates containing erythromycin. Such colonies are then inoculated into liquid medium without antibiotics, and propagated overnight at 30 °C. These cultures are used to inoculate further liquid cultures, without antibiotics, again propagated overnight at 30 °C. If needed, this is repeated one or more

35

times. Aliquots from each overnight culture are spread on plates with spectinomycin (120 $\mu\text{g/ml}$) and incubated overnight at 30 °C, then replica plated onto plates with erythromycin (5 $\mu\text{g/ml}$). Colonies able to grow on spectinomycin, but sensitive to erythromycin, are picked and further investigated, e.g. by southern analysis and growth experiments. Such colonies
5 will have the chromosomal gene encoding the small extracellular protein replaced by the *res-spc-res* cassette.

The spectinomycin resistance gene may subsequently be deleted from the strain by introduction of a plasmid expressing the pAM β 1 resolvase gene, as described in US
10 5,882,888.

Alternatively, the *res-spc-res* cassette may be deleted in its entirety using a plasmid containing just the joined upstream and downstream regions flanking the gene for the extracellular protein, or such a plasmid may be used directly in the first step to delete the
15 gene for the extracellular protein in the *B. licheniformis* strain.

CLAIMS

1. A *Bacillus licheniformis* mutant host cell derived from a parent *B. licheniformis* host cell, which mutant host cell is mutated in one or more gene(s) encoding one or more secreted polypeptide(s) which is at least 80% identical to one or more of the polypeptides shown in
5 SEQ ID NO's: 2 to 200, wherein the mutant host cell secretes at least 5% less of the one or more secreted polypeptide(s) than the parent host cell, when they are cultivated under comparable conditions.
2. The host cell according to claim 1, which is mutated by a partial or complete deletion of
10 the one or more gene(s) encoding the one or more secreted polypeptide(s).
3. The host cell according to claim 1 or 2, which is mutated by a partial or complete deletion of a gene encoding a secreted polypeptide which is at least 80% identical to the polypeptide shown in SEQ ID NO: 134.
15
4. The host cell according to any of claims 1 – 3, which is mutated in two or more genes encoding two or more secreted polypeptides.
5. The host cell according to any of claims 1 – 4, which comprises one or more heterologous
20 gene(s) encoding one or more heterologous polypeptide(s).
6. The host cell according to claim 5, wherein the heterologous gene(s) is present in at least two copies.
- 25 7. The host cell according to claim 5 or 6, wherein the heterologous gene(s) are stably integrated into the genome of the cell.
8. The host cell according to any of claims 5 - 7, wherein the heterologous gene(s) is integrated into the genome of the cell without leaving any antibiotic resistance marker genes
30 at the site of integration.
9. The host cell according to any of claims 5 - 8, wherein the heterologous gene(s) are transcribed from a heterologous promoter or from an artificial promoter.
- 35 10. The host cell according to any of claim 5 – 9, wherein the heterologous gene(s) are comprised in an operon, preferably a polycistronic operon.

11. The host cell according to any of claims 5 – 10, wherein the heterologous polypeptide(s) is an antimicrobial peptide, or a fusion peptide comprising a peptide part which in its native form has antimicrobial activity.

5 12. The host cell according to any of claims 5 – 10, wherein the heterologous polypeptide(s) has biosynthetic activity and produces a compound or an intermediate of interest.

13. The host cell according to claim 12, wherein the compound or intermediate of interest comprises vitamins, amino acids, antibiotics, carbohydrates, or surfactants.

10

14. The host cell according to claim 13, wherein the carbohydrates comprise hyaluronic acid.

15. The host cell according to any of claims 5 – 10, wherein the heterologous polypeptide(s) is an enzyme, preferably a secreted enzyme.

15

16. The host cell according to claim 15, wherein the enzyme is an enzyme of a class selected from the group of enzyme classes consisting of oxidoreductases (EC 1), transferases (EC 2), hydrolases (EC 3), lyases (EC 4), isomerases (EC 5), and ligases (EC 6).

20

17. The host cell according to claim 16, wherein the enzyme is an enzyme with an activity selected from the group of enzyme activities consisting of aminopeptidase, amylase, amyloglucosidase, mannanase, carbohydrase, carboxypeptidase, catalase, cellulase, chitinase, cutinase, cyclodextrin glycosyltransferase, deoxyribonuclease, esterase, galactosidase, beta-galactosidase, glucoamylase, glucose oxidase, glucosidase, haloperoxidase, hemicellulase, invertase, isomerase, laccase, ligase, lipase, lyase, mannosidase, oxidase, pectinase, peroxidase, phytase, phenoloxidase, polyphenoloxidase, protease, ribonuclease, transferase, transglutaminase, and xylanase.

25

30 18. The host cell according to claim 17, wherein the enzyme is an amylase or a mannanase.

19. A process for producing at least one product of interest in a *Bacillus licheniformis* mutant host cell, comprising cultivating a *B.licheniformis* mutant host cell as defined in any of the claims 1 - 18 in a suitable medium, whereby the said product is produced.

35

20. The process according to claim 19, further comprising isolating or purifying the product of interest.

21. A use of a *Bacillus licheniformis* mutant host cell as defined in any of the claims 1 - 18 for producing at least one product of interest comprising cultivating the mutant host cell in a suitable medium whereby the said product is produced.

5

22. The use according to claim 21 further comprising isolating or purifying the product of interest.

ABSTRACT

TITLE: Improved Bacillus Host Cell.

5 A *Bacillus licheniformis* mutant host cell derived from a parent *B. licheniformis* host cell, which mutant host cell is mutated in one or more gene(s) encoding one or more secreted polypeptide(s) which is at least 80% identical to one or more of the polypeptides shown in SEQ ID NO's: 2 to 200, wherein the mutant host cell secretes at least 5% less of the one or more secreted polypeptide(s) than the parent host cell, when they are cultivated under comparable conditions.

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Patent- og
Varemærkestyrelsen

10 APR. 2002

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Andersen, Jens Tønne
Clausen, Ib Groth
Jørgensen, Steen Troels
Olsen, Peter Bjarke
Rasmussen, Michael Dølberg

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1 5 10

acc atc aag acg ata cgc gca ttt ttg ttc atg gga gca ttg atg ctg 581
Thr Ile Lys Thr Ile Arg Ala Phe Leu Phe Met Gly Ala Leu Met Leu
15 20 25

atc ttc ctt tca atc gtt gtc atg acg gtg gtc ttg gcg gcc aaa tgg 629
Ile Phe Leu Ser Ile Val Val Met Thr Val Val Leu Ala Lys Trp
30 35 40

caa ggc gct cct tcg att cag gtg ccg agg tct acc gtg ctg tat gac 677
Gln Gly Ala Pro Ser Ile Gln Val Pro Arg Ser Thr Val Leu Tyr Asp
45 50 55

gga agc gga aag caa atg ggg gaa acg cat tac ggg caa aag cgg tac 725
Gly Ser Gly Lys Gln Met Gly Glu Thr His Tyr Gly Gln Lys Arg Tyr
60 65 70 75

tgg gtt tcg ctg aag aac atc aat ccc gca gtc atc gat gcc acg ctt 773
Trp Val Ser Leu Lys Asn Ile Asn Pro Ala Val Ile Asp Ala Thr Leu
80 85 90

gcc gtt gaa gac cgg aac ttt ttc cgg cac cac ggc ttt gac tat atg 821
Ala Val Glu Asp Arg Asn Phe Phe Arg His His Gly Phe Asp Tyr Met
95 100 105

agg atg ggc ggc gcc ctc att gcc gat tta aag gcg atg tcc aaa gtt 869
Arg Met Gly Gly Ala Leu Ile Ala Asp Leu Lys Ala Met Ser Lys Val
110 115 120

cag gga gcc agc acc atc acc cag caa tat gcg aga aac ctc tac ctc 917
Gln Gly Ala Ser Thr Ile Thr Gln Gln Tyr Ala Arg Asn Leu Tyr Leu
125 130 135

ggc cac gat aaa aca tgg aaa aga aag tgg aat gaa gct ttt tat acg 965
Gly His Asp Lys Thr Trp Lys Arg Lys Trp Asn Glu Ala Phe Tyr Thr
140 145 150 155

ata agg ctt gaa caa aac tac aca aag aaa gat att ttg gaa ggc tat 1013
Ile Arg Leu Glu Gln Asn Tyr Thr Lys Lys Asp Ile Leu Glu Gly Tyr
160 165 170

tta aat acg att tat tac ggg cat gga gca tac gga atc gaa gcg gct 1061
Leu Asn Thr Ile Tyr Tyr Gly His Gly Ala Tyr Gly Ile Glu Ala Ala
175 180 185

tcc cgg ctg tat ttt ggc aag cgg gcc aaa gat atc aat acg gcg gag 1109
Ser Arg Leu Tyr Phe Gly Lys Arg Ala Lys Asp Ile Asn Thr Ala Glu
190 195 200

gct gca atg ctt gcc ggc att cca aag ggt cct tca gtt tat tcg ccc 1157
Ala Ala Met Leu Ala Gly Ile Pro Lys Gly Pro Ser Val Tyr Ser Pro
205 210 215

ttt gtc aat gaa aaa aaa gcg aaa gaa cgc cag gaa atg atc ctg aca 1205
Phe Val Asn Glu Lys Lys Ala Lys Glu Arg Gln Glu Met Ile Leu Thr
220 225 230 235

atg atg gag aaa caa aac aag ctg acg gaa atg cag gcg gca gca ctg 1253
Met Met Glu Lys Gln Asn Lys Leu Thr Glu Met Gln Ala Ala Ala Leu
240 245 250

aaa aaa atg ccg ctc cgc ttt gaa aaa cag gat aag caa aca acc gaa 1301
Lys Lys Met Pro Leu Arg Phe Glu Lys Gln Asp Lys Gln Thr Thr Glu
255 260 265

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ttc acc acg ctc aac ccg cgt ctc caa aaa att gcc gag gat acg atc Phe Thr Thr Leu Asn Pro Arg Leu Gln Lys Ile Ala Glu Asp Thr Ile 300 305 310 315	1445
gaa cac acg ata gat tcg tca tcc gac att cag gcg gga ttt gca gcg Glu His Thr Ile Asp Ser Ser Ser Asp Gln Ala Gly Phe Ala Ala 320 325 330	1493
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tac gaa aaa agc cct ttt aac cgc gta acg cag gct atg cgg cag ccc Tyr Glu Lys Ser Pro Phe Asn Arg Val Thr Gln Ala Met Arg Gln Pro 350 355 360	1589
ggc tcc acc atg aag cct ttc ctt tat tat tcg gcg gtt caa aac ggc Gly Ser Thr Met Lys Pro Phe Leu Tyr Tyr Ser Ala Val Gln Asn Gly 365 370 375	1637
ttt aca ccg gcc acc cga atg agg agc gcg gaa acg aca ttt gag ctc Phe Thr Pro Ala Thr Arg Met Arg Ser Ala Glu Thr Thr Phe Glu Leu 380 385 390 395	1685
ggg caa ggc agc gct tat tcc ccg agc aac tat cac ggc tat tat gca Gly Gln Gly Ser Ala Tyr Ser Pro Ser Asn Tyr His Gly Tyr Tyr Ala 400 405 410	1733
gac ggt ccg atc acg ctt ctg cag gca ctg gct ttg tcc gat aac att Asp Gly Pro Ile Thr Leu Leu Gln Ala Leu Ala Leu Ser Asp Asn Ile 415 420 425	1781
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ctt gcg ctc gga aca tcc cct gtg aag ccg att gaa atg gtg aac gga Leu Ala Leu Gly Thr Ser Pro Val Lys Pro Ile Glu Met Val Asn Gly 460 465 470 475	1925
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cgg agc aaa caa atc ctt gac cca aaa gcg gct ttt atc acg gcg aac Arg Ser Lys Gln Ile Leu Asp Pro Lys Ala Ala Phe Ile Thr Ala Asn 510 515 520	2069
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ctt gct tca ggc gtg tgg acg gga tat gac aaa gag cgg aca atc gat Leu Ala Ser Gly Val Trp Thr Gly Tyr Asp Lys Glu Arg Thr Ile Asp 575 580 585	2261
gcc gtc gca gag aaa aac tat gcc aaa caa att tgg gct gag ttt atg Ala Val Ala Glu Lys Asn Tyr Ala Lys Gln Ile Trp Ala Glu Phe Met 590 595 600	2309
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ccc agc tgc ccg tcc aaa tat ttc gct tat ttt atc aaa ggt act gaa Pro Ser Cys Pro Ser Lys Tyr Phe Ala Tyr Phe Ile Lys Gly Thr Glu 640 645 650	2453
ccc gag cag gtt tgc tat gga aag gaa atc tat aag gag caa aac gcc Pro Glu Gln Val Cys Tyr Gly Lys Glu Ile Tyr Lys Glu Gln Asn Ala 655 660 665	2501
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<213> Bacillus licheniformis

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 35 40 45
 Ile Gln Val Pro Arg Ser Thr Val Leu Tyr Asp Gly Ser Gly Lys Gln
 50 55 60
 Met Gly Glu Thr His Tyr Gly Gln Lys Arg Tyr Trp Val Ser Leu Lys
 65 70 75 80
 Asn Ile Asn Pro Ala Val Ile Asp Ala Thr Leu Ala Val Glu Asp Arg
 85 90 95
 Asn Phe Phe Arg His His Gly Phe Asp Tyr Met Arg Met Gly Gly Ala
 100 105 110
 Leu Ile Ala Asp Leu Lys Ala Met Ser Lys Val Gln Gly Ala Ser Thr
 115 120 125
 Ile Thr Gln Gln Tyr Ala Arg Asn Leu Tyr Leu Gly His Asp Lys Thr
 130 135 140
 Trp Lys Arg Lys Trp Asn Glu Ala Phe Tyr Thr Ile Arg Leu Glu Gln
 145 150 155 160
 Asn Tyr Thr Lys Lys Asp Ile Leu Glu Gly Tyr Leu Asn Thr Ile Tyr
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 Tyr Gly His Gly Ala Tyr Gly Ile Glu Ala Ala Ser Arg Leu Tyr Phe
 180 185 190
 Gly Lys Arg Ala Lys Asp Ile Asn Thr Ala Glu Ala Ala Met Leu Ala
 195 200 205
 Gly Ile Pro Lys Gly Pro Ser Val Tyr Ser Pro Phe Val Asn Glu Lys
 210 215 220
 Lys Ala Lys Glu Arg Gln Glu Met Ile Leu Thr Met Met Glu Lys Gln
 225 230 235 240
 Asn Lys Leu Thr Glu Met Gln Ala Ala Ala Leu Lys Lys Met Pro Leu
 245 250 255
 Arg Phe Glu Lys Gln Asp Lys Gln Thr Thr Glu Lys Thr Ala Pro Tyr
 260 265 270
 Phe Tyr Asp Glu Ala Val Lys Glu Ile Ser Arg Leu Leu Arg Leu Thr
 275 280 285

Pro Glu Gln Ala Glu Thr Gly Gly Tyr Asn Val Phe Thr Thr Leu Asn
 290 295 300
 Pro Arg Leu Gln Lys Ile Ala Glu Asp Thr Ile Glu His Thr Ile Asp
 305 310 315 320
 Ser Ser Ser Asp Ile Gln Ala Gly Phe Ala Ala Ile Asn Pro Ser Asp
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 Gly Ser Val Leu Ala Leu Val Gly Gly Arg Asp Tyr Glu Lys Ser Pro
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 Phe Asn Arg Val Thr Gln Ala Met Arg Gln Pro Gly Ser Thr Met Lys
 355 360 365
 Pro Phe Leu Tyr Tyr Ser Ala Val Gln Asn Gly Phe Thr Pro Ala Thr
 370 375 380
 Arg Met Arg Ser Ala Glu Thr Thr Phe Glu Leu Gly Gln Gly Ser Ala
 385 390 395 400
 Tyr Ser Pro Ser Asn Tyr His Gly Tyr Tyr Ala Asp Gly Pro Ile Thr
 405 410 415
 Leu Leu Gln Ala Leu Ala Leu Ser Asp Asn Ile Tyr Ala Val Lys Thr
 420 425 430
 His Leu Phe Leu Gly Met Asp Lys Leu Ile Asp Ala Ala Lys Gln Phe
 435 440 445
 Gly Ile Asn Ser Pro Leu Gln Lys Val Pro Ser Leu Ala Leu Gly Thr
 450 455 460
 Ser Pro Val Lys Pro Ile Glu Met Val Asn Gly Tyr Ala Met Phe Ala
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 Asn Gly Gly Lys Lys Ile Glu Pro Ser Phe Ile Thr Lys Ile Thr Asp
 485 490 495
 Pro Asn Gly Lys Val Leu Tyr Glu Lys Pro Lys Arg Ser Lys Gln Ile
 500 505 510
 Leu Asp Pro Lys Ala Ala Phe Ile Thr Ala Asn Met Met Ser Gly Met
 515 520 525
 Phe Asp Lys Ser Leu Asn Gly Tyr Thr Ser Val Thr Gly Arg Thr Ile
 530 535 540
 Ala Asp Gln Leu Thr Arg Arg Tyr Ala Gly Lys Ser Gly Thr Thr Ser
 545 550 555 560

Thr Asp Ser Trp Met Ile Gly Phe Tyr Pro Gly Leu Ala Ser Gly Val
565 570 575

Trp Thr Gly Tyr Asp Lys Glu Arg Thr Ile Asp Ala Val Ala Glu Lys
580 585 590

Asn Tyr Ala Lys Gln Ile Trp Ala Glu Phe Met Glu Lys Ala Leu Glu
595 600 605

Asp Ala Pro Ala Ala Ala Leu Met Pro Pro Glu Gly Val Lys Gly Met
610 615 620

Tyr Ile Asp Pro Ala Thr Gly Tyr Ala Ala Ala Pro Ser Cys Pro Ser
625 630 635 640

Lys Tyr Phe Ala Tyr Phe Ile Lys Gly Thr Glu Pro Glu Gln Val Cys
645 650 655

Tyr Gly Lys Glu Ile Tyr Lys Glu Gln Asn Ala Gly His Glu Lys Pro
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Lys Gly Glu
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gtcatcggcc cggtgctcgg cggcatcctt tccagctttt tcggtatttc ttccgccttt 180
tacgcaactg cagtcctctt tttcggcgga gcatgccttc tgatgttcca aagggtcccag 240
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attatccttc tcgatatcca aaaagaatgg tacgatatgg ctagaattta gcgaaaagag 360

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Val Thr Lys Leu Arg Ser Phe Phe Gly Trp Ile Phe Leu Leu Met Leu
1 5 10 15

ata cct ata ttt gtc ttt acc tta atg gcc tcc ggc cgg gaa gct cag 457
Ile Pro Ile Phe Val Phe Thr Leu Met Ala Ser Gly Arg Glu Ala Gln
20 25 30

aat atg aag cct ctc gat cag gtg ctc gat gag aag atc aat ata aag 505
Asn Met Lys Pro Leu Asp Gln Val Leu Asp Glu Lys Ile Asn Ile Lys
35 40 45

gat atc ggc ctt gta caa aac agc tac atg tat gac agg gac ggc gct 553
Asp Ile Gly Leu Val Gln Asn Ser Tyr Met Tyr Asp Arg Asp Gly Ala
50 55 60

ctg att tcc gaa atc gtt tca gat cac caa aac cgg gta ttc gtc ccc 601
Leu Ile Ser Glu Ile Val Ser Asp His Gln Asn Arg Val Phe Val Pro
65 70 75 80

tat aaa gat atc cct gaa cat gtg aag cag ctg ttt ctg act tcg gag 649
Tyr Lys Asp Ile Pro Glu His Val Lys Gln Leu Phe Leu Thr Ser Glu
85 90 95

gac cgt cat ttc ttt cag cat aaa ggc ttt gat ttt atc ggg atg gcc 697
Asp Arg His Phe Phe Gln His Lys Gly Phe Asp Phe Ile Gly Met Ala
100 105 110

cgg gcc gcc gca gcc aat gtc aaa aaa ggc ggc att gat cag ggg gcc 745
Arg Ala Ala Ala Asn Val Lys Lys Gly Gly Ile Asp Gln Gly Ala
115 120 125

agc acg att aca cag cag ctt tcg aga aac ttg tat ttg aac cat gaa 793
Ser Thr Ile Thr Gln Gln Leu Ser Arg Asn Leu Tyr Leu Asn His Glu
130 135 140

cga acc ttc gac cgc aag ttc act gag ctc ctg tat tcc tac cag ctg 841
Arg Thr Phe Asp Arg Lys Phe Thr Glu Leu Leu Tyr Ser Tyr Gln Leu
145 150 155 160

gaa aaa aag ctt tca aaa gaa gaa att ttt gag aaa tac tta aac acc 889
Glu Lys Lys Leu Ser Lys Glu Glu Ile Phe Glu Lys Tyr Leu Asn Thr
165 170 175

atc tat ttt aat cac ggg gtc tac gga att gga tcc gcg tct tct ttc 937
Ile Tyr Phe Asn His Gly Val Tyr Gly Ile Gly Ser Ala Ser Ser Phe
180 185 190

tat ttc agc aag cct ttg aaa tct ctc agc ctt gcc gaa acg gcg ttt 985
Tyr Phe Ser Lys Pro Leu Lys Ser Leu Ser Leu Ala Glu Thr Ala Phe
195 200 205

att tgc gcg atc cct aat aac cct aca tta tat gat cct ttg aaa cat 1033
Ile Cys Ala Ile Pro Asn Asn Pro Thr Leu Tyr Asp Pro Leu Lys His
210 215 220

ttt gac tac aca aaa acc cgc caa aag cgg ctg ctt gaa ggg ctg aaa 1081
Phe Asp Tyr Thr Lys Thr Arg Gln Lys Arg Leu Leu Glu Gly Leu Lys
225 230 235 240

aaa gcg ggc gtg atc acc gaa aaa gaa tac agc aaa gcc gtt aag caa 1129
Lys Ala Gly Val Ile Thr Glu Lys Glu Tyr Ser Lys Ala Val Lys Gln
245 250 255

aaa att acg ctt aac gtg aaa gaa aag aaa gac gac tat ccc gac tat 1177

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Lys	Ile	Thr	Leu	Asn	Val	Lys	Glu	Lys	Lys	Asp	Asp	Tyr	Pro	Asp	Tyr		
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ggg	ttt	gac	gaa	cgg	ctg	aaa	aag	gca	aaa	aca	aaa	gaa	gaa	aag	aaa	1273	
Gly	Phe	Asp	Glu	Arg	Leu	Lys	Lys	Ala	Lys	Thr	Lys	Glu	Glu	Lys	Lys		
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Lys	Ile	Glu	Lys	Glu	Leu	Ser	Asn	Arg	Ile	Ser	Ser	Leu	Thr	Thr	Ser		
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Gly	Ile	Lys	Ile	Tyr	Thr	Ala	Leu	Asp	Thr	Ser	Met	Gln	Asn	Arg	Val		
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Val	Gln	Gln	Val	Lys	Asn	Arg	Leu	Pro	Tyr	Glu	Gly	Val	Gln	Gly	Gly		
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Ala	Val	Val	Ile	Asn	His	Gln	Thr	His	Gln	Ile	Val	Ala	Met	Ser	Gly		
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ggg	aaa	aac	tat	aaa	aag	tac	gat	tat	aac	ctg	gca	ttc	caa	gca	tac	1513	
Gly	Lys	Asn	Tyr	Lys	Lys	Tyr	Asp	Tyr	Asn	Leu	Ala	Phe	Gln	Ala	Tyr		
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Arg	Gln	Pro	Gly	Ser	Ser	Ile	Lys	Pro	Leu	Leu	Asp	Tyr	Gly	Pro	Tyr		
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Ile	Glu	Glu	Thr	Gly	Ala	Thr	Ala	Gly	Ser	Met	Ile	Asp	Ala	Ser	Lys		
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Phe	Cys	Ser	Lys	Glu	Tyr	Cys	Pro	Asn	Asn	Phe	Asn	Glu	Arg	Thr	Tyr		
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Gly	Thr	Val	Ser	Ile	Lys	Thr	Ala	Phe	Lys	Tyr	Ser	Tyr	Asn	Thr	Pro		
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gcc	gta	cgt	atg	ctg	aac	cgg	gtc	ggc	gtg	caa	aaa	gga	ttc	agc	tat	1753	
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Leu	Lys	Pro	Phe	Gly	Phe	Asp	Lys	Ile	Val	Gln	Asn	Asp	Tyr	Arg	Leu		
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cct	gct	gcg	ctg	ggc	gga	ttt	aca	tgg	ggc	ttc	tca	ccg	ctg	gag	atg	1849	
Pro	Ala	Ala	Leu	Gly	Gly	Phe	Thr	Trp	Gly	Phe	Ser	Pro	Leu	Glu	Met		
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gct	gat	gcc	tat	acg	acc	ttc	ggc	aat	aac	gga	agc	tac	aca	tcc	agc	1897	
Ala	Asp	Ala	Tyr	Thr	Thr	Phe	Gly	Asn	Asn	Gly	Ser	Tyr	Thr	Ser	Ser		
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cat	gca	atc	aca	aag	gtg	acg	gat	tta	aaa	gga	aaa	acg	cta	tac	aaa	1945	
His	Ala	Ile	Thr	Lys	Val	Thr	Asp	Leu	Lys	Gly	Lys	Thr	Leu	Tyr	Lys		
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atg cgc gaa ctc tta gca gcg gtt gtt aaa gaa gga acc gga aaa aaa 2041
Met Arg Glu Leu Leu Ala Ala Val Val Lys Glu Gly Thr Gly Lys Lys
545 550 555 560

gcg aat ttc agc ggc gga tat gta gga gga aaa acc gga aca tcc aac 2089
Ala Asn Phe Ser Gly Gly Tyr Val Gly Gly Lys Thr Gly Thr Ser Asn
565 570 575

ggg tac aga gac ctt tgg ttt gtc gga ttg acg gat aca tac aca atg 2137
Gly Tyr Arg Asp Leu Trp Phe Val Gly Leu Thr Asp Thr Tyr Thr Met
580 585 590

agt gta tgg gtc gga aaa gag gca aaa ggc act gtc gag tac ctg cat 2185
Ser Val Trp Val Gly Lys Glu Ala Lys Gly Thr Val Glu Tyr Leu His
595 600 605

cac gcg gga cct caa ctt tta atc tgg aga gga acg ctg caa tac gca 2233
His Ala Gly Pro Gln Leu Leu Ile Trp Arg Gly Thr Leu Gln Tyr Ala
610 615 620

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Ser
625

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<213> Bacillus licheniformis

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Asn Met Lys Pro Leu Asp Gln Val Leu Asp Glu Lys Ile Asn Ile Lys
35 40 45

Asp Ile Gly Leu Val Gln Asn Ser Tyr Met Tyr Asp Arg Asp Gly Ala
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 Leu Ile Ser Glu Ile Val Ser Asp His Gln Asn Arg Val Phe Val Pro
 65 70 75 80
 Tyr Lys Asp Ile Pro Glu His Val Lys Gln Leu Phe Leu Thr Ser Glu
 85 90 95
 Asp Arg His Phe Phe Gln His Lys Gly Phe Asp Phe Ile Gly Met Ala
 100 105 110
 Arg Ala Ala Ala Ala Asn Val Lys Lys Gly Gly Ile Asp Gln Gly Ala
 115 120 125
 Ser Thr Ile Thr Gln Gln Leu Ser Arg Asn Leu Tyr Leu Asn His Glu
 130 135 140
 Arg Thr Phe Asp Arg Lys Phe Thr Glu Leu Leu Tyr Ser Tyr Gln Leu
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 Glu Lys Lys Leu Ser Lys Glu Glu Ile Phe Glu Lys Tyr Leu Asn Thr
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Ser
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Met Lys Arg Phe Leu Gln Cys Ala Leu Ile Ala
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ctg	aat	gaa	acg	aca	aaa	caa	gtc	gcg	ttt	act	caa	acg	tcg	ctg	tgg	2309
Leu	Asn	Glu	Thr	Thr	Lys	Gln	Val	Ala	Phe	Thr	Gln	Thr	Ser	Leu	Trp	
		590					595					600				
gat	tca	aat	tac	tcg	atg	gct	gtt	ttc	gcg	ccg	ttt	aaa	ggg	caa	ggc	2357
Asp	Ser	Asn	Tyr	Ser	Met	Ala	Val	Phe	Ala	Pro	Phe	Lys	Gly	Gln	Gly	
	605					610					615					
aca	gca	gtc	aca	aaa	gaa	atg	atc	aac	ttt	ttg	aac	agc	aat	gat	ttc	2405
Thr	Ala	Val	Thr	Lys	Glu	Met	Ile	Asn	Phe	Leu	Asn	Ser	Asn	Asp	Phe	
					625					630					635	
gca	gca	acc	gtt	gtg	aat	gaa	acg	gac	agc	cat	cag	cta	ttt	aca	aac	2453
Ala	Ala	Thr	Val	Val	Asn	Glu	Thr	Asp	Ser	His	Gln	Leu	Phe	Thr	Asn	
				640					645					650		
cat	caa	cag	ctg	aca	gca	aaa	tcc	gcc	gaa	acc	aag	acg	gat	gat	aaa	2501
His	Gln	Gln	Leu	Thr	Ala	Lys	Ser	Ala	Glu	Thr	Lys	Thr	Asp	Asp	Lys	
			655					660					665			
cag	gaa	agc	aat	cag	cag	cat	gtg	ctg	tac	att	gcc	atc	ctg	atc	gta	2549

Gln Glu Ser Asn Gln Gln His Val Leu Tyr Ile Ala Ile Leu Ile Val
 670 675 680

atc ata gcg gca gcg gtt att ttg atc ttg aca acg gca agg cgc aga 2597
 ile ile Ala Ala Ala Val ile Leu ile Leu Thr Thr Ala Arg Arg Arg
 685 690 695

aaa aga aag gcc aat gcc ggc gga ggg att gac gaa taaaacaggg 2643
 Lys Arg Lys Ala Asn Ala Gly Gly Gly ile Asp Glu
 700 705 710

gcttgctttt agcccctggt tttttataag tattcaacct gtttctcata tacacccttc 2703
 gcaatttttag ctaaaacatc gattccccctt ataatatctt catccgccgc ggtaggctg 2763
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 20 25 30

Gly Ser Ile Leu Gly Glu Asn Ser Arg Glu Gln Ala Lys Gln Gln Val
 35 40 45

Leu Thr Asn Asp Leu Leu Thr Leu Tyr Gly Ala Lys Asp Ser Ala Glu
 50 55 60

Leu Thr Tyr Gln Ile Pro Ala Gly Ala Ser Ser Thr His Gln Gln Leu
 65 70 75 80

Thr Leu Lys Tyr Glu Ala Ser Asp Leu Leu Ile Ser Pro Ser Ser Leu
 85 90 95

Thr Ala Glu Ile Asp Gly Glu Pro Val Lys Thr Val Lys Leu Glu Gly
 100 105 110

Asn Asn Gly Lys Lys Thr Leu Lys Leu Ser Leu Asn Lys Ser Gln Ser
 115 120 125

Ser Pro Gly Phe His Ser Leu Ser Leu Lys Phe Tyr Gly Val Val His
 130 135 140

Glu Gly Val Cys Val Arg Gln Asp Ser Ser Gly Asn Trp Ile Lys Ile
 145 150 155 160

Tyr Pro Asp Ser Arg₁₆₅ Leu Asn Ile Gly₁₇₀ Glu Lys Asn Glu Ser₁₇₅ Lys Gly
 Ala Ala Leu Glu₁₈₀ His Tyr Pro Tyr₁₈₅ Phe Ala Gln Ser₁₉₀ Gly Ser Ser
 Val Glu Lys₁₉₅ Thr Ala Ile Val₂₀₀ Ile Pro Asp His Pro₂₀₅ Ser Ser Ala Glu
 Ile Glu₂₁₀ Ala Ala Val Lys₂₁₅ Thr Glu Ala Tyr Leu Lys₂₂₀ Thr Val Asp Asn
 Ser₂₂₅ Ile Ser Thr Lys₂₃₀ Ile Leu Gly Glu Ser₂₃₅ Asp Leu Ala Lys Ile Asp₂₄₀
 Arg Pro Thr Ile Val₂₄₅ Ile Gly Val His₂₅₀ His Trp Ser Gly₂₅₅ Lys Val
 Lys Lys Leu₂₆₀ Lys Lys Gln Ala Lys₂₆₅ Glu Ala Lys Glu Asp₂₇₀ Lys Leu
 Leu Leu Ala₂₇₅ Lys Arg Met Leu₂₈₀ Lys Ala Lys Asp Lys₂₈₅ Gln Gln Pro Val
 Leu Phe₂₉₀ Ala Ala Ala Ala Ser₂₉₅ Asp Asp Val Leu₃₀₀ Ser Glu Lys Ile Ser
 Val₃₀₅ Ile Thr Asp Lys₃₁₀ Thr Tyr Ala Ala Gln Leu₃₁₅ Ser Gly Asp Thr Leu₃₂₀
 Ala Ile Gly Lys₃₂₅ Leu Gln Gln His Ser₃₃₀ Lys Arg Gly Gly Ser₃₃₅ Lys Leu
 Thr Leu Glu Asp₃₄₀ Phe Gly Ala Gly₃₄₅ Asp Leu Thr Ile Gly Ser₃₅₀ Gly Gln
 Thr Ser Ser₃₅₅ Glu His Phe Tyr Tyr₃₆₀ Pro Ala Pro Ala Leu₃₆₅ Leu Asp Lys
 Asn Gln₃₇₀ Pro Ala Lys Leu Ser₃₇₅ Leu Ala Met Lys Lys₃₈₀ Ser Lys Thr Ile
 Gln Lys Gln Ala Gly₃₉₀ Gln Ser Asp Leu Ala Ala₃₉₅ Glu Gln Ala Glu Leu₄₀₀
 Lys Val Met Ile Asn₄₀₅ Gly Gln Pro His Ser₄₁₀ Val Gly Leu Asp Asp₄₁₅ Ile
 Gly Lys Glu Asp₄₂₀ Lys Asn Gly Phe Tyr₄₂₅ His Val Ser Leu Lys₄₃₀ Val Asp

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Pro Lys Leu₄₃₅ Leu Gln Lys Ser Arg₄₄₀ Tyr Ile Asp Ile Gln₄₄₅ Phe Ala Ala
 Ser Gly₄₅₀ Leu Lys Glu Asn Asn₄₅₅ Pro Cys Tyr Ala Val₄₆₀ Asn Glu Asp Lys
 Trp₄₆₅ Ile Phe Ile Asp Lys₄₇₀ Gln Ser Ala Leu Ser₄₇₅ Tyr His Val Ser Asp₄₈₀
 Thr Ser Ala Ser Ala₄₈₅ Asp Phe Gln Ala Trp₄₉₀ Pro Leu Pro Tyr Ala₄₉₅ Gly
 Asp His Asn Asn₅₀₀ Lys Thr Leu Met Ile₅₀₅ Leu Pro Asp Asn Ala₅₁₀ Asp Gln
 Ser Lys Ile₅₁₅ Asp Glu Leu Ser Leu₅₂₀ Val Val Gly Ser Phe₅₂₅ Gly Ser Glu
 Ala Arg₅₃₀ Gln Ala Phe Thr Val₅₃₅ Lys Thr Ser Ser Glu₅₄₀ Val Lys Pro Asp
 Asp Val₅₄₅ Lys Gly Arg Asn₅₅₀ Val Ile Phe Ile Gly₅₅₅ Ser Val Asp Gln Phe₅₆₀
 Ser Leu Leu Lys Glu₅₆₅ Lys Thr Ala Glu Leu₅₇₀ Ala Val Pro Thr Ala₅₇₅ Lys
 Asn Gly Thr Phe₅₈₀ Asp Val Ser Ser Phe₅₈₅ Gln Met Leu Asn Glu₅₉₀ Thr Thr
 Lys Gln Val₅₉₅ Ala Phe Thr Gln Thr Ser Leu Trp Asp Ser₆₀₅ Asn Tyr Ser
 Met Ala₆₁₀ Val Phe Ala Pro Phe₆₁₅ Lys Gly Gln Gly Thr₆₂₀ Ala Val Thr Lys
 Glu Met Ile Asn Phe Leu₆₃₀ Asn Ser Asn Asp Phe₆₃₅ Ala Ala Thr Val Val₆₄₀
 Asn Glu Thr Asp Ser₆₄₅ His Gln Leu Phe Thr₆₅₀ Asn His Gln Gln Leu Thr₆₅₅
 Ala Lys Ser Ala₆₆₀ Glu Thr Lys Thr Asp₆₆₅ Asp Lys Gln Glu Ser Asn Gln
 Gln His Val₆₇₅ Leu Tyr Ile Ala Ile₆₈₀ Leu Ile Val Ile Ile₆₈₅ Ala Ala Ala
 Val Ile₆₉₀ Leu Ile Leu Thr Thr₆₉₅ Ala Arg Arg Arg Lys₇₀₀ Arg Lys Ala Asn

Ala Gly Gly Gly Ile Asp Glu
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<211> 2431

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (519)..(1958)

<223>

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atccatctat gtttgagcct gtgcacggct ctgctccgga catcatctga tagcgagtca 180
tcatcggaaa aggaatcgcc aatccgatcg gccaaatttg gacggcaaaa atgatgctcg 240
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agagcggcta cttaacgcct gatatcggcg gttcaagtac gacggatgat gtgacagaag 360
aaatcatcaa gcgcgtgagg accatataag cgaaagctgc cagcactccg gcagcttttt 420
ttgctgtgga atggaaaatc gattacatga tacggggcgg tttggcgcat actacatcaa 480
gcaacaaaac atagtgcagg cagaagagga ggtatagg atg aat cag aag att gtg 536
Met Asn Gln Lys Ile Val
1 5

tct gtg ctc atc att gcg ctc agc ctg tta tgc ggc ttg gta aca ggc 584
Ser Val Leu Ile Ile Ala Leu Ser Leu Leu Cys Gly Leu Val Thr Gly
10 15 20

gcc ggc ccg att ccg tta cat gat gtc gtt tca aaa gca tca gcg gct 632
Ala Gly Pro Ile Pro Leu His Asp Val Val Ser Lys Ala Ser Ala Ala
25 30 35

gaa gaa gct gca gcc aaa agc acc gct aga aac gaa ttg gag aaa att 680
Glu Glu Ala Ala Ala Lys Ser Thr Ala Arg Asn Glu Leu Glu Lys Ile
40 45 50

gag aaa gca tat gac ctg att tca aat gaa tat gtg gag cag gtc gac 728
Glu Lys Ala Tyr Asp Leu Ile Ser Asn Glu Tyr Val Glu Gln Val Asp
55 60 65 70

agg gaa aaa ctg ttg gaa gga gcc ata cag ggc atg ctt tca aca ttg 776
Arg Glu Lys Leu Leu Glu Gly Ala Ile Gln Gly Met Leu Ser Thr Leu
75 80 85

aat gac cca tac tcg gtc tat atg gat aaa cag acg gca aag cgg ttt 824

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Asn	Asp	Pro	Tyr	Ser	Val	Tyr	Met	Asp	Lys	Gln	Thr	Ala	Lys	Arg	Phe	
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Ser	Asp	Ser	Leu	Asp	Ser	Ser	Phe	Glu	Gly	Ile	Gly	Ala	Glu	Ile	Gly	
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atg	gaa	gac	aga	aaa	atc	att	atc	ggt	tct	cct	ttt	aaa	cag	tct	ccg	920
Met	Glu	Asp	Arg	Lys	Ile	Ile	Ile	Val	Ser	Pro	Phe	Lys	Gln	Ser	Pro	
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gca	gag	aaa	gcc	gga	tta	aag	ccg	aac	gat	gaa	atc	att	agc	atc	gac	968
Ala	Glu	Lys	Ala	Gly	Leu	Lys	Pro	Asn	Asp	Glu	Ile	Ile	Ser	Ile	Asp	
135				140						145					150	
ggc	gat	tcc	atg	agc	gga	atg	gat	ttg	aat	gac	gcc	gta	tta	aag	atc	1016
Gly	Asp	Ser	Met	Ser	Gly	Met	Asp	Leu	Asn	Asp	Ala	Val	Leu	Lys	Ile	
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aga	ggc	aaa	aag	gga	tcg	acg	ggt	aca	ctg	aaa	ggt	cac	cga	ccc	gga	1064
Arg	Gly	Lys	Lys	Gly	Ser	Thr	Val	Thr	Leu	Lys	Val	His	Arg	Pro	Gly	
			170					175					180			
atg	aaa	gac	cag	ctg	aca	ttt	acg	att	aag	cgc	gat	gaa	atc	ccg	ctg	1112
Met	Lys	Asp	Gln	Leu	Thr	Phe	Thr	Ile	Lys	Arg	Asp	Glu	Ile	Pro	Leu	
		185					190					195				
gaa	acg	gtg	ttt	gct	tcc	ata	aag	aaa	gta	cag	gat	aaa	cct	gtc	ggc	1160
Glu	Thr	Val	Phe	Ala	Ser	Ile	Lys	Lys	Val	Gln	Asp	Lys	Pro	Val	Gly	
	200					205					210					
tat	atc	gca	ata	tct	tcc	ttt	tcc	gaa	cat	acg	gca	aaa	gat	ttt	act	1208
Tyr	Ile	Ala	Ile	Ser	Ser	Phe	Ser	Glu	His	Thr	Ala	Lys	Asp	Phe	Thr	
215					220					225					230	
gct	gaa	ctg	aaa	aag	ctt	gag	aaa	aag	gga	ata	aaa	ggg	ctc	gtt	ttg	1256
Ala	Glu	Leu	Lys	Lys	Leu	Glu	Lys	Lys	Gly	Ile	Lys	Gly	Leu	Val	Leu	
				235					240					245		
gat	gta	aga	gga	aat	ccg	ggc	ggg	tac	ttg	caa	agc	gtg	gaa	gac	att	1304
Asp	Val	Arg	Gly	Asn	Pro	Gly	Gly	Tyr	Leu	Gln	Ser	Val	Glu	Asp	Ile	
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tta	aaa	cat	ttt	gtg	aca	aaa	gat	cat	ccg	tat	ata	caa	atc	gcc	gaa	1352
Leu	Lys	His	Phe	Val	Thr	Lys	Asp	His	Pro	Tyr	Ile	Gln	Ile	Ala	Glu	
		265					270					275				
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cca	tac	cct	gtg	agc	gtg	atc	acg	gac	aag	ggc	agc	gct	tcg	gct	tcg	1448
Pro	Tyr	Pro	Val	Ser	Val	Ile	Thr	Asp	Lys	Gly	Ser	Ala	Ser	Ala	Ser	
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gaa	att	ctt	gca	ggc	gca	tta	aaa	gaa	gcc	gag	ggc	tac	gac	gtg	gtt	1496
Glu	Ile	Leu	Ala	Gly	Ala	Leu	Lys	Glu	Ala	Glu	Gly	Tyr	Asp	Val	Val	
				315					320					325		
ggc	gat	cct	tcc	ttt	gga	aag	gga	acc	gtc	cag	cag	gcg	gtg	ccg	atg	1544
Gly	Asp	Pro	Ser	Phe	Gly	Lys	Gly	Thr	Val	Gln	Gln	Ala	Val	Pro	Met	
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gga	gac	ggt	agc	aat	att	aag	ctg	acg	ctg	tac	aaa	tgg	ctg	aca	cct	1592
Gly	Asp	Gly	Ser	Asn	Ile	Lys	Leu	Thr	Leu	Tyr	Lys	Trp	Leu	Thr	Pro	
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Lys Gly Asn Trp Ile His Lys Gln Gly Ile Gln Pro Thr Val Pro Val
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 acg cag cct gca tat ttc tcg gcg ggg cct tta cag ctg aaa gaa ccc 1688
 Thr Gln Pro Ala Tyr Phe Ser Ala Gly Pro Leu Gln Leu Lys Glu Pro 390
 375 380
 ctc aag ccg gat atg aac aac aat gaa att aag cgg gcg cag ttc ctg 1736
 Leu Lys Pro Asp Met Asn Asn Asn Glu Ile Lys Arg Ala Gln Phe Leu 405
 395 400
 ctg aaa gga ctc ggg ttt gtc ccc ggc cgg gaa gac ggc tat tac aat 1784
 Leu Lys Gly Leu Gly Phe Val Pro Gly Arg Glu Asp Gly Tyr Tyr Asn 420
 410 415
 gaa agc aca aaa aaa gcc gtc atg gcg ttt cag gca gca aac aag ctg 1832
 Glu Ser Thr Lys Lys Ala Val Met Ala Phe Gln Ala Ala Asn Lys Leu 435
 425 430
 aag caa aca ggg atc att gac caa aaa acg gca aat aca atg aac ctg 1880
 Lys Gln Thr Gly Ile Ile Asp Gln Lys Thr Ala Asn Thr Met Asn Leu 450
 440 445
 cgg att gag gag aaa aag atg gat gaa aag aac gat ctt cag ctg caa 1928
 Arg Ile Glu Glu Lys Lys Met Asp Glu Lys Asn Asp Leu Gln Leu Gln 470
 455 460 465
 gcc gca tta aaa gtg ctg ttt aac aaa aag tgagggcacg ggatgtcctc 1978
 Ala Ala Leu Lys Val Leu Phe Asn Lys Lys 480
 475 480
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<212> PRT

<213> Bacillus licheniformis

<400> 12

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Ser Lys Ala Ser Ala Ala Glu Glu Ala Ala Ala Lys Ser Thr Ala Arg
 35 40 45

Asn Glu Leu Glu Lys Ile Glu Lys Ala Tyr Asp Leu Ile Ser Asn Glu
 50 55 60

Tyr Val Glu Gln Val Asp Arg Glu Lys Leu Leu Glu Gly Ala Ile Gln
 65 70 75 80

Gly Met Leu Ser Thr Leu Asn Asp Pro Tyr Ser Val Tyr Met Asp Lys
 85 90 95

Gln Thr Ala Lys Arg Phe Ser Asp Ser Leu Asp Ser Ser Phe Glu Gly
 100 105 110

Ile Gly Ala Glu Ile Gly Met Glu Asp Arg Lys Ile Ile Ile Val Ser
 115 120 125

Pro Phe Lys Gln Ser Pro Ala Glu Lys Ala Gly Leu Lys Pro Asn Asp
 130 135 140

Glu Ile Ile Ser Ile Asp Gly Asp Ser Met Ser Gly Met Asp Leu Asn
 145 150 155 160

Asp Ala Val Leu Lys Ile Arg Gly Lys Lys Gly Ser Thr Val Thr Leu
 165 170 175

Lys Val His Arg Pro Gly Met Lys Asp Gln Leu Thr Phe Thr Ile Lys
 180 185 190

Arg Asp Glu Ile Pro Leu Glu Thr Val Phe Ala Ser Ile Lys Lys Val
 195 200 205

Gln Asp Lys Pro Val Gly Tyr Ile Ala Ile Ser Ser Phe Ser Glu His
 210 215 220

Thr Ala Lys Asp Phe Thr Ala Glu Leu Lys Lys Leu Glu Lys Lys Gly
 225 230 235 240

Ile Lys Gly Leu Val Leu Asp Val Arg Gly Asn Pro Gly Gly Tyr Leu
 245 250 255

Gln Ser Val Glu Asp Ile Leu Lys His Phe Val Thr Lys Asp His Pro
 260 265 270

Tyr Ile Gln Ile Ala Glu Arg Asn Gly Asn Lys Lys Gln Tyr Phe Ser
 275 280 285

Lys Leu Lys Glu Lys Lys Pro Tyr Pro Val Ser Val Ile Thr Asp Lys
 290 295 300

Gly Ser Ala Ser Ala Ser Glu Ile Leu Ala Gly Ala Leu Lys Glu Ala
 305 310 315 320

Glu Gly Tyr Asp Val Val Gly Asp Pro Ser Phe Gly Lys Gly Thr Val
 325 330 335

Gln Gln Ala Val Pro Met Gly Asp Gly Ser Asn Ile Lys Leu Thr Leu
 340 345 350

Tyr Lys Trp Leu Thr Pro Lys Gly Asn Trp Ile His Lys Gln Gly Ile
 355 360 365

Gln Pro Thr Val Pro Val Thr Gln Pro Ala Tyr Phe Ser Ala Gly Pro
 370 375 380

Leu Gln Leu Lys Glu Pro Leu Lys Pro Asp Met Asn Asn Asn Glu Ile
 385 390 395 400

Lys Arg Ala Gln Phe Leu Leu Lys Gly Leu Gly Phe Val Pro Gly Arg
 405 410 415

Glu Asp Gly Tyr Tyr Asn Glu Ser Thr Lys Lys Ala Val Met Ala Phe
 420 425 430

Gln Ala Ala Asn Lys Leu Lys Gln Thr Gly Ile Ile Asp Gln Lys Thr
 435 440 445

Ala Asn Thr Met Asn Leu Arg Ile Glu Glu Lys Lys Met Asp Glu Lys
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<211> 2542

<212> DNA

<213> Bacillus licheniformis

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<223>

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ccgacagaat atacgaattc aaaagcgtcg gcaattcctc gaccctcccg catgacagca	420
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agaagggacg ttagac atg gca aaa caa caa ata ggt gta gtt ggt tta gca	1012
Met Ala Lys Gln Gln Ile Gly Val Val Gly Leu Ala	
1 5 10	
gta atg gga aaa aac ttg gct tta aac att gaa agc cgc ggg ttt tca	1060
Val Met Gly Lys Asn Leu Ala Leu Asn Ile Glu Ser Arg Gly Phe Ser	
15 20 25	
gtt tct gtc tac aac aga tca agc gag aaa acc gaa gag ttt ctg aaa	1108
Val Ser Val Tyr Asn Arg Ser Ser Glu Lys Thr Glu Glu Phe Leu Lys	
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gaa gcc gaa ggc aaa aac gtt gtc ggt aca tac agc att gaa gag ttt	1156
Glu Ala Glu Gly Lys Asn Val Val Gly Thr Tyr Ser Ile Glu Glu Phe	
45 50 55 60	
gtt gaa tct ctt gaa aaa ccg cgc aaa att ctt tta atg gtc aaa gct	1204
Val Glu Ser Leu Glu Lys Pro Arg Lys Ile Leu Leu Met Val Lys Ala	
65 70 75	
gga aca ccg aca gac gca acg att caa tcg ctt ctg cct cat ctt gaa	1252
Gly Thr Pro Thr Asp Ala Thr Ile Gln Ser Leu Leu Pro His Leu Glu	
80 85 90	
aaa ggc gac att ttg att gac ggc gga aat aca tat tat aaa gat acg	1300
Lys Gly Asp Ile Leu Ile Asp Gly Gly Asn Thr Tyr Tyr Lys Asp Thr	
95 100 105	
cag aga aga aac agg gag ctg gcc gaa agc ggc att cac ttc atc ggc	1348
Gln Arg Arg Asn Arg Glu Leu Ala Glu Ser Gly Ile His Phe Ile Gly	
110 115 120	
acc ggc gtt tcc ggc ggt gaa gaa ggc gct ctg aaa ggg ccg tct atc	1396
Thr Gly Val Ser Gly Gly Glu Glu Gly Ala Leu Lys Gly Pro Ser Ile	
125 130 135 140	
atg cca ggc gga caa aag gaa gcc cat gag ctt gtc aag ccg att ctt	1444
Met Pro Gly Gly Gln Lys Glu Ala His Glu Leu Val Lys Pro Ile Leu	
145 150 155	

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ggc cct gac ggc gcc ggc cat tat gta aaa atg gtt cat aac ggc atc Gly Pro Asp 175 Gly Ala Gly His 180 Tyr Val Lys Met Val 185 His Asn Gly Ile	1540
gaa tac ggc gat atg cag ctg atc tca gaa tcc tac ttt att ttg aaa Glu Tyr 190 Gly Asp Met Gln 195 Leu Ile Ser Glu Ser 200 Tyr Phe Ile Leu Lys	1588
cac att gtc ggt ctg tca tca gat gag ctt cac gaa gtc ttt tcc gag His Ile Val Gly Leu 210 Ser Ser Asp Glu Leu 215 His Glu Val Phe Ser 220 Glu	1636
tgg aat aag gga gag ctt gac agc tat ctg atc gaa atc acg gct gat Trp Asn Lys Gly 225 Glu Leu Asp Ser Tyr 230 Leu Ile Glu Ile Thr 235 Ala Asp	1684
att ttc acg aaa aaa gac gag gaa acc ggc aag ccg ctt gtt gac gtc Ile Phe Thr Lys 240 Lys Asp Glu Glu 245 Thr Gly Lys Pro Leu Val 250 Asp Val	1732
atc ctc gat aaa gca ggt caa aaa ggc aca gga aaa tgg aca agc caa Ile Leu Asp 255 Lys Ala Gly Gln 260 Lys Gly Thr Gly Lys 265 Trp Thr Ser Gln	1780
agc gct ctt gac ctg ggc gtt ccg ctt cca atc att acg gaa tct gtt Ser Ala 270 Leu Asp Leu Gly 275 Val Pro Leu Pro Ile 280 Thr Glu Ser Val	1828
ttc gcc cgc ttc atc tct tcc atg aaa gag gag cgc gtc aaa gcg agc Phe Ala 285 Arg Phe Ile Ser 290 Ser Met Lys Glu Glu 295 Arg Val Lys Ala Ser 300	1876
aag ctt ctg gca gga cct gaa gcg aaa cct gcc gct gag aac aaa gaa Lys Leu Leu Ala 305 Gly Pro Glu Ala Lys 310 Pro Ala Ala Glu Asn Lys 315 Glu	1924
gag ctg atc gaa gcg gtc aga aaa gcg ctc ttc atg agc aaa atc tgt Glu Leu Ile Glu Ala Val Arg Lys Ala 325 Leu Phe Met Ser Lys 330 Ile Cys	1972
tct tac gcc caa ggc ttt gct caa atg aaa gcc gca tca gaa gaa tac Ser Tyr 335 Ala Gln Gly Phe Ala Gln Met Lys Ala Ala Ser 345 Glu Glu Tyr	2020
ggc tgg gat ttg aaa tac ggc gat atc gcg atg att ttc cgc gga gga Gly Trp 350 Asp Leu Lys Tyr Gly 355 Asp Ile Ala Met Ile 360 Phe Arg Gly Gly	2068
tgc atc atc cgc gcg gcg ttc ctg caa aaa atc aaa gaa gcg tat gac Cys Ile 365 Ile Arg Ala Ala Phe Leu Gln Lys Ile 375 Lys Glu Ala Tyr Asp 380	2116
cgc gat cca gag ctt gac aac ctg ctt ctt gac ccg tac ttc aaa aat Arg Asp Pro Glu Leu 385 Asp Asn Leu Leu 390 Asp Pro Tyr Phe Lys 395 Asn	2164
atc gtt gaa agc tat cag gga gcc ctc cgc aaa acg att tct ctt gcg Ile Val Glu Ser 400 Tyr Gln Gly Ala Leu 405 Arg Lys Thr Ile Ser Leu Ala	2212
gtt gaa caa gga att cct gta cct tgc ttc tca agc gct ctc gct tac Val Glu 415 Gly Ile Pro Val Pro 420 Cys Phe Ser Ser 425 Ala Leu Ala Tyr	2260

10294.000.ST25.txt

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Phe Asp Ser Tyr Arg Thr Ala Thr Leu Pro Ala Asn Leu Ile Gln Ala
430          435          440

cag cgc gac tac ttt ggc gcc cat acg tat gag cgt aca gat aaa gaa      2356
Gln Arg Asp Tyr Phe Gly Ala His Thr Tyr Glu Arg Thr Asp Lys Glu
445          450          455          460

ggc att ttc cac act gag tgg atg aaa taagatgtaa aaccgcaagc      2403
Gly Ile Phe His Thr Glu Trp Met Lys
465

tgaaaagctt gcggtttttt tgattttcgg aaggatgcat gtttaagcgg ttgtgtggaa      2463

acctactcaa aagtgagttt caataaggag gaatcaaccc atgtatccaa gtttagaggg      2523

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<210> 14

<211> 469

<212> PRT

<213> Bacillus licheniformis

<400> 14

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Asn Leu Ala Leu Asn Ile Glu Ser Arg Gly Phe Ser Val Ser Val Tyr
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Asn Arg Ser Ser Glu Lys Thr Glu Glu Phe Leu Lys Glu Ala Glu Gly
35          40          45

Lys Asn Val Val Gly Thr Tyr Ser Ile Glu Glu Phe Val Glu Ser Leu
50          55          60

Glu Lys Pro Arg Lys Ile Leu Leu Met Val Lys Ala Gly Thr Pro Thr
65          70          75          80

Asp Ala Thr Ile Gln Ser Leu Leu Pro His Leu Glu Lys Gly Asp Ile
85          90          95

Leu Ile Asp Gly Gly Asn Thr Tyr Tyr Lys Asp Thr Gln Arg Arg Asn
100          105          110

Arg Glu Leu Ala Glu Ser Gly Ile His Phe Ile Gly Thr Gly Val Ser
115          120          125

Gly Gly Glu Glu Gly Ala Leu Lys Gly Pro Ser Ile Met Pro Gly Gly
130          135          140

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Gln Lys Glu Ala His Glu Leu Val Lys Pro Ile Leu Glu Ala Ile Ser
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 Ala Lys Val Asp Gly Glu Pro Cys Thr Thr Tyr Ile Gly Pro Asp Gly
 165 170 175
 Ala Gly His Tyr Val Lys Met Val His Asn Gly Ile Glu Tyr Gly Asp
 180 185 190
 Met Gln Leu Ile Ser Glu Ser Tyr Phe Ile Leu Lys His Ile Val Gly
 195 200 205
 Leu Ser Ser Asp Glu Leu His Glu Val Phe Ser Glu Trp Asn Lys Gly
 210 215 220
 Glu Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala Asp Ile Phe Thr Lys
 225 230 235 240
 Lys Asp Glu Glu Thr Gly Lys Pro Leu Val Asp Val Ile Leu Asp Lys
 245 250 255
 Ala Gly Gln Lys Gly Thr Gly Lys Trp Thr Ser Gln Ser Ala Leu Asp
 260 265 270
 Leu Gly Val Pro Leu Pro Ile Ile Thr Glu Ser Val Phe Ala Arg Phe
 275 280 285
 Ile Ser Ser Met Lys Glu Glu Arg Val Lys Ala Ser Lys Leu Leu Ala
 290 295 300
 Gly Pro Glu Ala Lys Pro Ala Ala Glu Asn Lys Glu Glu Leu Ile Glu
 305 310 315 320
 Ala Val Arg Lys Ala Leu Phe Met Ser Lys Ile Cys Ser Tyr Ala Gln
 325 330 335
 Gly Phe Ala Gln Met Lys Ala Ala Ser Glu Glu Tyr Gly Trp Asp Leu
 340 345 350
 Lys Tyr Gly Asp Ile Ala Met Ile Phe Arg Gly Gly Cys Ile Ile Arg
 355 360 365
 Ala Ala Phe Leu Gln Lys Ile Lys Glu Ala Tyr Asp Arg Asp Pro Glu
 370 375 380
 Leu Asp Asn Leu Leu Leu Asp Pro Tyr Phe Lys Asn Ile Val Glu Ser
 385 390 395 400
 Tyr Gln Gly Ala Leu Arg Lys Thr Ile Ser Leu Ala Val Glu Gln Gly
 405 410 415

Ile Pro Val Pro Cys Phe Ser Ser Ala Leu Ala Tyr Phe Asp Ser Tyr
 420 425 430

Arg Thr Ala Thr Leu Pro Ala Asn Leu Ile Gln Ala Gln Arg Asp Tyr
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Phe Gly Ala His Thr Tyr Glu Arg Thr Asp Lys Glu Gly Ile Phe His
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Thr Glu Trp Met Lys
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<210> 15

<211> 2030

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1391)

<223>

<400> 15

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ctgaaatcga cgtgttgatc ccgggcgccca aacgcgctga tcagctgacg gacaacctca 180

aaacggcaga agtcaatctg tctcaagagg acattgattt catcgaccgg ctgtttgccc 240

gctaaatgat caggaaacct atcttaaaag ataggtttct ttatttttaa aatcctgttg 300

acagcgcttc catttttgat atgataggaa agaagttaat acaagtgacg gagaatggga 360

gattcacaaat aagaccctct tgtgccaggg gtttttttgt ggatctcttt ttcttcgtca 420

tctaagagggg ggcgaaagca atcgtaatga atagacggca cttttattct gtataacagc 480

ttgaaaggag agatcatgtt atg aaa aga cta gtc cgc agc atc ttc ctt ata 533
 Met Lys Arg Leu Val Arg Ser Ile Phe Leu Ile
 1 5 10

acg gcc gca atc gct gct ttt ggt ttt gga ttc agc ggg cat gcg gag 581
 Thr Ala Ala Ile Ala Ala Phe Gly Phe Gly Phe Ser Gly His Ala Glu
 15 20 25

gcg gca agc cat tcc cag ccg cag ctc aat ccg aac aag cta cta aat 629
 Ala Ala Ser His Ser Gln Pro Gln Leu Asn Pro Asn Lys Leu Leu Asn
 30 35 40

gtc gcg cac cgc ggc gca tcg ggg cat gct ccc gag cac acg ctt ttg 677
 Val Ala His Arg Gly Ala Ser Gly His Ala Pro Glu His Thr Leu Leu
 45 50 55

10294.000.ST25.txt

gct tat aag ctt gga caa aaa atg aaa ggc gat tac ata gaa atc gat Ala Tyr Lys Leu Gly Gln Lys Met Lys Gly Asp Tyr Ile Glu Ile Asp 60 65 70 75	725
ctt caa atg aca aaa gac ggc cac ttg gtc gcc atg cac gat gag aca Leu Gln Met Thr Lys Asp Gly His Leu Val Ala Met His Asp Glu Thr 80 85 90	773
ttg gat cgt acg act aat ggt acg ggt ttt gtc aaa gac tat acg ctg Leu Asp Arg Thr Thr Asn Gly Thr Gly Phe Val Lys Asp Tyr Thr Leu 95 100 105	821
aaa gaa atc aaa gag ctt gat gca ggc tcc tgg ttt aac gaa gca tat Lys Glu Ile Lys Glu Leu Asp Ala Gly Ser Trp Phe Asn Glu Ala Tyr 110 115 120	869
cct gag cgg gca aaa ccg gag tac gcc ggg ctg aaa gtg ccc acc ctt Pro Glu Arg Ala Lys Pro Glu Tyr Ala Gly Leu Lys Val Pro Thr Leu 125 130 135	917
gaa gaa atc atc caa aca ttc ggg aga agc gcg cgc tac tat atc gaa Glu Glu Ile Ile Gln Thr Phe Gly Arg Ser Ala Arg Tyr Tyr Ile Glu 140 145 150 155	965
aca aaa tca ccg gaa gac tat gat cat atg gaa gaa aag ctc ctg gac Thr Lys Ser Pro Glu Asp Tyr Asp His Met Glu Glu Lys Leu Leu Asp 160 165 170	1013
atc ctg aag caa tac aaa ttg acc gga gca gac att cat tca agc aaa Ile Leu Lys Gln Tyr Lys Leu Thr Gly Ala Asp Ile His Ser Ser Lys 175 180 185	1061
gtc atc att caa tct ttt agt cct gaa agc tta aaa atc att cat aac Val Ile Ile Gln Ser Phe Ser Pro Glu Ser Leu Lys Ile Ile His Asn 190 195 200	1109
gct aat cca aac att ccg cta gtg caa tta tta tgg tac gac aaa cct Ala Asn Pro Asn Ile Pro Leu Val Gln Leu Leu Trp Tyr Asp Lys Pro 205 210 215	1157
gct gcc att act gac gcc gaa tta aaa caa tat caa tct tac agc gtc Ala Ala Ile Thr Asp Ala Glu Leu Lys Gln Tyr Gln Ser Tyr Ser Val 220 225 230 235	1205
gga ctc ggc atg aac ttt gac cgc att ggc cgg gca tac gtg caa aag Gly Leu Gly Met Asn Phe Asp Arg Ile Gly Arg Ala Tyr Val Gln Lys 240 245 250	1253
att cga cgc acc ggc atg ctg gtc cat cct tat act gtg aat aaa aaa Ile Arg Arg Thr Gly Met Leu Val His Pro Tyr Thr Val Asn Lys Lys 255 260 265	1301
gaa gat atg aag cgg ctg ctc gat tgg gga gcg acc gga atg ttc acc Glu Asp Met Lys Arg Leu Leu Asp Trp Gly Ala Thr Gly Met Phe Thr 270 275 280	1349
aac ttt ccg gac cgg ctg cgc gat gtt ttg cgc gaa aag aag Asn Phe Pro Asp Arg Leu Arg Asp Val Leu Arg Glu Lys Lys 285 290 295	1391
taaataaata aagaagggga ataccatgtt aaaactgttt aagccagcac cgccgattga	1451
gcggctgccg gaagatcaaa ttgattcgga atataagaaa ttcagactgc aagtttttct	1511
cggcattctt atcgggttatg cggcatacta ttttaattcgc aaaaatttct cgcttgccat	1571
gccttatttg atcgaagagg gcttttcaaa gtcggcgctc ggctttgcct tgtccgctct	1631

10294.000.ST25.txt

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tgttcctttt ttcacctcat cgatcgccat tatgtttatc atgctgttct taaacggctg 1811
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<210> 16

<211> 297

<212> PRT

<213> Bacillus licheniformis

<400> 16

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20 25 30

Gln Pro Gln Leu Asn Pro Asn Lys Leu Leu Asn Val Ala His Arg Gly
35 40 45

Ala Ser Gly His Ala Pro Glu His Thr Leu Leu Ala Tyr Lys Leu Gly
50 55 60

Gln Lys Met Lys Gly Asp Tyr Ile Glu Ile Asp Leu Gln Met Thr Lys
65 70 75 80

Asp Gly His Leu Val Ala Met His Asp Glu Thr Leu Asp Arg Thr Thr
85 90 95

Asn Gly Thr Gly Phe Val Lys Asp Tyr Thr Leu Lys Glu Ile Lys Glu
100 105 110

Leu Asp Ala Gly Ser Trp Phe Asn Glu Ala Tyr Pro Glu Arg Ala Lys
115 120 125

Pro Glu Tyr Ala Gly Leu Lys Val Pro Thr Leu Glu Glu Ile Ile Gln
130 135 140

Thr Phe Gly Arg Ser Ala Arg Tyr Tyr Ile Glu Thr Lys Ser Pro Glu
145 150 155 160

Asp Tyr Asp His Met Glu Glu Lys Leu Leu Asp Ile Leu Lys Gln Tyr
 165 170 175

Lys Leu Thr Gly Ala Asp Ile His Ser Ser Lys Val Ile Ile Gln Ser
 180 185 190

Phe Ser Pro Glu Ser Leu Lys Ile Ile His Asn Ala Asn Pro Asn Ile
 195 200 205

Pro Leu Val Gln Leu Leu Trp Tyr Asp Lys Pro Ala Ala Ile Thr Asp
 210 215 220

Ala Glu Leu Lys Gln Tyr Gln Ser Tyr Ser Val Gly Leu Gly Met Asn
 225 230 235 240

Phe Asp Arg Ile Gly Arg Ala Tyr Val Gln Lys Ile Arg Arg Thr Gly
 245 250 255

Met Leu Val His Pro Tyr Thr Val Asn Lys Lys Glu Asp Met Lys Arg
 260 265 270

Leu Leu Asp Trp Gly Ala Thr Gly Met Phe Thr Asn Phe Pro Asp Arg
 275 280 285

Leu Arg Asp Val Leu Arg Glu Lys Lys
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<210> 17

<211> 2308

<212> DNA

<213> Bacillus licheniformis

<220>

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<222> (501)..(1814)

<223>

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aacggggatc cttttgaatg caaaggtcag ctctgagcta ttgatcaaca tctttattcc	180
gaacactccg cttcatgacg gagccgtgat tatgaaaaac gatgagggtg ctgcagctgc	240
ctgctacctt ccgctttctg aaagcccttt tatttcaaaa gagcttggaa cgaggcacag	300
agcagcagtg ggaatcagtg aagtgaccga cagtctgacg gttgttgtat ccgaagagac	360

10294.000.ST25.txt

gggcggcatc agcgtcgcca aaaacggaga ccttcaccgt gatttatcgg aagaggcatt	420
gaaaaatatg cttgaagcgg aattttaagaa aaattcgcgg gaaacttcct caaatcgctg	480
gtattggagg gCGaagaaaa atg gat aag ttc tta aac aat ccc tgg gct gtc Met Asp Lys Phe Leu Asn Asn Pro Trp Ala Val 1 5 10	533
aaa gtt gtc gCG tta ttg ttc gCG ttt ctt ctt tac ttt gCG gtc cac Lys Val Val Ala Leu Leu Phe Ala Phe Leu Leu Tyr Phe Ala Val His 15 20 25	581
agc gct cag gCG ccg act ccg aag aaa cca ggt gaa tcg ttt ttc ccg Ser Ala Gln Ala Pro Thr Pro Lys Lys Pro Gly Glu Ser Phe Phe Pro 30 35 40	629
aca tcg aca aca gac gaa gCG acg ctc acc gat ata ccg gtc aaa tcg Thr Ser Thr Thr Asp Glu Ala Thr Leu Thr Asp Ile Pro Val Lys Ser 45 50 55	677
ttt tat gat gat gaa aac tac gtc gta aca gCG gtg ccg cag acg gtg Phe Tyr Asp Asp Glu Asn Tyr Val Val Thr Gly Val Pro Gln Thr Val 60 65 70 75	725
aat gtc acg att aaa gCG ccg acc gga acc gtc aag aag gtc aga caa Asn Val Thr Ile Lys Gly Pro Thr Gly Thr Val Lys Lys Val Arg Gln 80 85 90	773
gtg aag gat ttt gag att tat gcc gac atg caa aac ctg aaa aca gCG Val Lys Asp Phe Glu Ile Tyr Ala Asp Met Gln Asn Leu Lys Thr Gly 95 100 105	821
agg cat aaa gtc gag ctg aag gcc aga aat gtt gcc gac gCG ctc act Arg His Lys Val Glu Leu Lys Ala Arg Asn Val Ala Asp Gly Leu Thr 110 115 120	869
ctg acc atc aat cca tcg gtg aca acc gtg acg atc gaa gaa aaa acg Leu Thr Ile Asn Pro Ser Val Thr Thr Val Thr Ile Glu Glu Lys Thr 125 130 135	917
acg aag gaa ttc ccg gtc gag gtt gat ttt tat aat aaa aac aaa atg Thr Lys Glu Phe Pro Val Glu Val Asp Phe Tyr Asn Lys Asn Lys Met 140 145 150 155	965
aaa gac gCG tac acg ccg gag ctg ccg atc atc aac ccg aaa aac gtc Lys Asp Gly Tyr Thr Pro Glu Leu Pro Ile Ile Asn Pro Lys Asn Val 160 165 170	1013
agc gtc acc gCG tca aaa gcc gtg atc gac aga atc cag aac atc aag Ser Val Thr Gly Ser Lys Ala Val Ile Asp Arg Ile Gln Asn Ile Lys 175 180 185	1061
gCG acg atc aat tta gag gCG gtc gac cag acg gtt gaa aaa gaa gcc Ala Thr Ile Asn Leu Glu Gly Val Asp Gln Thr Val Glu Lys Glu Ala 190 195 200	1109
aag ctt aca gta tac gac aag gac gga aat gtc ctg ccg gtt gaa gtc Lys Leu Thr Val Tyr Asp Lys Asp Gly Asn Val Leu Pro Val Glu Val 205 210 215	1157
agc cct tcc gtc gtt aaa atc acc gtt ccg gtg acg agc ccg agc aaa Ser Pro Ser Val Val Lys Ile Thr Val Pro Val Thr Ser Pro Ser Lys 220 225 230 235	1205
aag att ccg gtc aaa gtt gac cgg aaa gCG agc ctt ccg gac gCG atc Lys Ile Pro Val Lys Val Asp Arg Lys Gly Ser Leu Pro Asp Gly Ile 240 245 250	1253

10294.000.ST25.txt

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ccg caa aat gtt ctt gat tgc tta gaa ttt gtc gag gcc gac gag att Pro Gln Asn Val Leu Asp Ser Leu Glu Phe Val Glu Ala Asp Glu Ile	1349
gat tta agt aaa ata aag gat gat act gaa ttg gaa gcc ggc att aaa Asp Leu Ser Lys Ile Lys Asp Asp Thr Glu Leu Glu Ala Gly Ile Lys	1397
gtg ccg gac ggc gct aaa aag gtg tca ccc gaa aaa gtg aaa atc aag Val Pro Asp Gly Ala Lys Lys Val Ser Pro Glu Lys Val Lys Ile Lys	1445
gtg aaa gtt gac aag gaa gaa gag aaa aaa ctg aaa aac gtt tca att Val Lys Val Asp Lys Glu Glu Glu Lys Lys Leu Lys Asn Val Ser Ile	1493
aaa acc gcg ggg ctg aat gac agc cgg gat ctt gaa ttt ctc gat ccg Lys Thr Ala Gly Leu Asn Asp Ser Arg Asp Leu Glu Phe Leu Asp Pro	1541
aag tca gcg aag ctg gat atc acg gca aag ggc tcg aca gcc gcg atc Lys Ser Gly Lys Leu Asp Ile Thr Ala Lys Gly Ser Thr Ala Ala Ile	1589
gaa aaa ctc cag cct tcc gac gtc gag ctc tat gtc aat gtg gcg gat Glu Lys Leu Gln Pro Ser Asp Val Glu Leu Tyr Val Asn Val Ala Asp	1637
ctc gat gac ggc gag cac aat gta aag ctg gaa gta aac ggt ccg cag Leu Asp Asp Gly Glu His Asn Val Lys Leu Glu Val Asn Gly Pro Gln	1685
aac atg aca tgg tcg ctg ccg cgg caa agc att cga gtg aaa atc tca Asn Met Thr Trp Ser Leu Pro Arg Gln Ser Ile Arg Val Lys Ile Ser	1733
tct caa aca acc caa aac gaa aaa aac aat ggt cag gat gaa gaa gaa Ser Gln Thr Thr Gln Asn Glu Lys Asn Asn Gly Gln Asp Glu Glu Glu	1781
gag aat cat tct gaa aag gat tca caa cct tca tgaatcaaaa aggagcgata Glu Asn His Ser Glu Lys Asp Ser Gln Pro Ser	1834
ttaatgggca agtatttttg tacagacggt gtaagaggcg tggcaaacag tgaacttaca	1894
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tccgatgaac aggagcttga aatcgagcgt ctgatggatc agccggaaga tcacctgcca	2254
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<212> PRT

<213> Bacillus Ticheniformis

<400> 18

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Thr Pro Lys Lys Pro Gly Glu Ser Phe Phe Pro Thr Ser Thr Thr Asp
 35 40 45

Glu Ala Thr Leu Thr Asp Ile Pro Val Lys Ser Phe Tyr Asp Asp Glu
 50 55 60

Asn Tyr Val Val Thr Gly Val Pro Gln Thr Val Asn Val Thr Ile Lys
 65 70 75 80

Gly Pro Thr Gly Thr Val Lys Lys Val Arg Gln Val Lys Asp Phe Glu
 85 90 95

Ile Tyr Ala Asp Met Gln Asn Leu Lys Thr Gly Arg His Lys Val Glu
 100 105 110

Leu Lys Ala Arg Asn Val Ala Asp Gly Leu Thr Leu Thr Ile Asn Pro
 115 120 125

Ser Val Thr Thr Val Thr Ile Glu Glu Lys Thr Thr Lys Glu Phe Pro
 130 135 140

Val Glu Val Asp Phe Tyr Asn Lys Asn Lys Met Lys Asp Gly Tyr Thr
 145 150 155 160

Pro Glu Leu Pro Ile Ile Asn Pro Lys Asn Val Ser Val Thr Gly Ser
 165 170 175

Lys Ala Val Ile Asp Arg Ile Gln Asn Ile Lys Ala Thr Ile Asn Leu
 180 185 190

Glu Gly Val Asp Gln Thr Val Glu Lys Glu Ala Lys Leu Thr Val Tyr
 195 200 205

Asp Lys Asp Gly Asn Val Leu Pro Val Glu Val Ser Pro Ser Val Val
 210 215 220

Lys Ile Thr Val Pro Val Thr Ser Pro Ser Lys Lys Ile Pro Val Lys
 225 230 235 240

Val Asp Arg Lys Gly Ser Leu Pro Asp Gly Ile Ser Ile Ser Ser Leu
 245 250 255
 Asp Ile Ser Pro Gly Glu Val Thr Val Tyr Gly Pro Gln Asn Val Leu
 260 265 270
 Asp Ser Leu Glu Phe Val Glu Ala Asp Glu Ile Asp Leu Ser Lys Ile
 275 280 285
 Lys Asp Asp Thr Glu Leu Glu Ala Gly Ile Lys Val Pro Asp Gly Ala
 290 295 300
 Lys Lys Val Ser Pro Glu Lys Val Lys Ile Lys Val Lys Val Asp Lys
 305 310 315 320
 Glu Glu Glu Lys Lys Leu Lys Asn Val Ser Ile Lys Thr Ala Gly Leu
 325 330 335
 Asn Asp Ser Arg Asp Leu Glu Phe Leu Asp Pro Lys Ser Gly Lys Leu
 340 345 350
 Asp Ile Thr Ala Lys Gly Ser Thr Ala Ala Ile Glu Lys Leu Gln Pro
 355 360 365
 Ser Asp Val Glu Leu Tyr Val Asn Val Ala Asp Leu Asp Asp Gly Glu
 370 375 380
 His Asn Val Lys Leu Glu Val Asn Gly Pro Gln Asn Met Thr Trp Ser
 385 390 395 400
 Leu Pro Arg Gln Ser Ile Arg Val Lys Ile Ser Ser Gln Thr Thr Gln
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<210> 19

<211> 2632

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (852)..(2606)

<223>

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 cggcaagcgt ttttccccgt gtaaccggga cccttctgat ctgataatct cccatgagat 180
 cgaccgcttt tcaatgaatg tttacactta ccgtaatgat agaaggggccc tttggatatg 240
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 aacgattaag g atg agg aag cat tta ctg ata gct gtc tgt act ttg gca 890
 Met Arg Lys His Leu Leu Ile Ala Val Cys Thr Leu Ala
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 Pro Thr Thr Ala Asp Ser Pro Gln Ser Ser Gly Phe Phe Val Asp His
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 Tyr Lys Asn Asn Ile Ser Ala Asn Thr Thr Ala Glu Ser Asn Pro Val
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 Ile Gly Leu Leu Ser Glu Phe Asn Lys Leu Trp Thr Pro Gly Lys Thr
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 Trp Asn Thr Gly Thr Lys Leu Asn Ser Arg Val Leu Asp Ala Asn Ile
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 Gln Lys Val Val Asp Ile Ala Glu Arg Arg Thr Met Leu Glu Glu Asn
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 gct gcc tat ttt gat gat cgg cgg agc cag agc tac agt ata att gac 1226
 Ala Ala Tyr Phe Asp Asp Arg Arg Ser Gln Ser Tyr Ser Ile Ile Asp
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Phe	Asp	Glu	Ala	Arg	Arg	Lys	Leu	Leu	Thr	Gln	Thr	Gly	Thr	Ala	Glu		
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 Glu Gly Asp Asn Thr Tyr Ser Gly Gly Thr Arg Ile Asp Gln Gly Thr
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 Gly Asp Tyr Lys Gln Ser Ala Lys Gly Ile Leu Glu Leu Gln Leu Ser
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Gly Lys Glu Thr Val Ile Glu Gln Ala Asp Thr Val Glu His Val Tyr
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Glu Leu Glu His Asp Pro Asp Val Leu Tyr Val Glu Asp Asn Leu Pro
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Asn	Lys	Lys	Val	Ser	Ala	Ala	Lys	Ala	Lys	Val	Lys	Thr	Ala	Glu	Gln	
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				560					565					570		
ctg	aaa	gca	tcc	gcc	gaa	aaa	acg	aag	ctg	caa	aaa	cgg	atc	aat	gcc	2261
Leu	Lys	Ala	Ser	Ala	Glu	Lys	Thr	Lys	Leu	Gln	Lys	Arg	Ile	Asn	Ala	
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Ile	Lys	Leu	Lys													
		590														
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gcggctgtca	aagctgtgga	tccggtgtc	cccaggacg	aagtactcgt	tttcaggcac											2556
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10294.000.ST25.txt

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<212> PRT

<213> Bacillus licheniformis

<400> 22

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Asn Glu Val Ile Val Val Tyr Lys Asn Thr Ser Gly Lys Glu Thr Val
35 40 45

Ile Glu Gln Ala Asp Thr Val Glu His Val Tyr Arg His Ile Pro Ala
50 55 60

Ala Ala Val Thr Ala Asp Asp Lys Thr Val Arg Glu Leu Glu His Asp
65 70 75 80

Pro Asp Val Leu Tyr Val Glu Asp Asn Leu Pro Val Ala Ala Ala Asp
85 90 95

Ser Thr Ala Leu Lys Ala Phe Ser Ser Ser Thr Ala Gln Asn Ala Ser
100 105 110

Ala Phe Ser Gln Trp Asn Ile Lys Leu Ile Gln Ala Ala Leu Ala Trp
115 120 125

Asn Lys Gly Leu Thr Gly Lys Gln Val Lys Ile Ala Val Ile Asp Ser
130 135 140

Gly Ile Ser Pro His Glu Glu Leu Ser Ile Ala Gly Gly Ala Ser Met
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Val Gly Tyr Thr Ala Ser Tyr Arg Asp Asp Asn Gly His Gly Thr His
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Val Ala Gly Ile Ile Gly Ala Lys His Asn Gly Arg Gly Ile Asp Gly
180 185 190

Ile Ala Pro Gly Ala Gln Leu Tyr Ala Val Lys Ala Leu Asp Arg Asn
 195 200 205
 Gly Ala Gly Asp Leu Lys Gly Ile Leu Gln Gly Ile Asp Trp Ser Ile
 210 215 220
 Gln His Gly Ile Asp Ile Ile Asn Met Ser Leu Val Val Ser Gly Asp
 225 230 235 240
 Ser Gln Val Leu His Asp Ala Val Asp Lys Ala Tyr Lys Arg Gly Ile
 245 250 255
 Ile Leu Val Gly Ala Ser Gly Asn Ala Gly Asn Gly Lys Ser Val Tyr
 260 265 270
 Tyr Pro Ala Ala Tyr Ser Ser Val Ile Ala Val Ser Ala Thr Asn Glu
 275 280 285
 Lys Asn Gln Ile Ala Ser Phe Thr Asn Thr Arg Ser Ala Val Ser Tyr
 290 295 300
 Ser Ala Pro Ser Thr Ser Ile Ile Asn Thr Ser Gly Asn Arg Gly Tyr
 305 310 315 320
 Ala Ile Gly Ser Cys Thr Ala Gln Gly Thr Pro Asp Val Thr Cys Val
 325 330 335
 Ile Ala Leu Met Lys Gln Leu His Pro Thr Ala Ser Asn Ala Glu Leu
 340 345 350
 Arg Lys Lys Met Gln Phe Tyr Thr Ser Asp Leu Gly Ala Pro Gly Arg
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 Asp His Leu Phe Gly Tyr Arg Leu Ile Arg Phe Lys Glu Val Thr Gln
 370 375 380
 Pro Leu Glu Lys Ala Gln Lys Ala Val Gly Gln Ala Glu Lys Thr Lys
 385 390 395 400
 Lys Lys Ala Asp Ile Gln Thr Ala Gln Lys Ala Ile Glu Pro Leu Pro
 405 410 415
 Ala Asp Ala Asp Lys Pro Ala Leu Lys Lys Arg Leu Asn Thr Val Lys
 420 425 430
 Glu Gln Leu Lys Lys Thr Ala Glu Ser Lys Val Lys Leu Ala Glu Lys
 435 440 445
 Gln Lys Lys Lys Thr Asn Ala Asp Ser Ala Gln Lys Ala Val Asn Glu
 450 455 460

10294.000.ST25.txt

Leu Asp Ser Gly Thr Phe Lys Thr Asn Leu Gln Lys Arg Ile Asn Ala
465 470 475 480

Val Arg Ser Ser Leu Leu Lys Thr Ala Lys Gln Ala Val Ala Lys Ala
485 490 495

Glu Lys Ala Ala Thr Asp Ser Asn Leu Gly Lys Ala Gln Lys Ala Ile
500 505 510

Asn Glu Leu Pro Ala Gly Lys Asp Lys Ser Asn Leu Gln Lys Arg Leu
515 520 525

Asn Thr Ala Lys Lys Gln Ala Ala Ala Tyr Asn Lys Lys Val Ser
530 535 540

Ala Ala Lys Ala Lys Val Lys Thr Ala Glu Gln Lys Arg Thr Lys Lys
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Thr Lys Ser Ala Ala Gln Ser Ala Val Gly Lys Leu Lys Ala Ser Ala
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Glu Lys Thr Lys Leu Gln Lys Arg Ile Asn Ala Ile Lys Leu Lys
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<211> 2347

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (513)..(1856)

<223>

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10294.000.ST25.txt

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Leu	Leu	Leu	Leu	Thr	Cys	Phe	Phe	Pro	Leu	Pro	Ser	Thr	Ala	Gln	Thr		
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gcc	atc	ggg	aac	gag	aca	aaa	cag	cgg	ctg	aca	tat	cct	gtt	tta	acg		629
Ala	Ile	Gly	Asn	Glu	Thr	Lys	Gln	Arg	Leu	Thr	Tyr	Pro	Val	Leu	Thr		
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aaa	gcg	aaa	acg	cct	gaa	gaa	gcc	ggt	ttt	tct	tcg	aaa	aag	ctt	aaa		677
Lys	Ala	Lys	Thr	Pro	Glu	Glu	Ala	Gly	Phe	Ser	Ser	Lys	Lys	Leu	Lys		
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gct	gcc	ctt	att	ttg	att	aaa	gac	gga	aaa	atc	atc	aaa	aaa	gaa	gtc		773
Ala	Ala	Leu	Ile	Leu	Ile	Lys	Asp	Gly	Lys	Ile	Ile	Lys	Lys	Glu	Val		
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Tyr	Gly	Tyr	Lys	Gln	Lys	Tyr	Asn	Gly	Leu	Ile	Ala	Leu	Lys	His	Pro		
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aaa	aaa	atg	aaa	gca	aac	acg	atg	ttc	gac	cta	gcc	tcc	aat	aca	aaa		869
Lys	Lys	Met	Lys	Ala	Asn	Thr	Met	Phe	Asp	Leu	Ala	Ser	Asn	Thr	Lys		
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Met	Tyr	Ala	Val	Asn	Phe	Ala	Leu	Gln	His	Leu	Val	Ser	Thr	Gly	Lys		
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Leu	Asp	Leu	Asn	Lys	Asn	Ile	Ser	Gln	Tyr	Leu	Pro	Asp	Phe	Lys	Asp		
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His	Pro	Glu	Asp	Asp	Val	Lys	Gly	Lys	Asn	Arg	Leu	Arg	Val	Ile	Asp		
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Glu	Tyr	Leu	Val	Lys	Thr	Pro	Leu	Ala	Tyr	Glu	Pro	Gly	Thr	Lys	Gln		
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Ile	Tyr	Ser	Asp	Ile	Asp	Tyr	Met	Leu	Leu	Gly	Leu	Ile	Ile	Glu	Lys		
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Ile	Thr	Asn	Glu	Arg	Leu	Asp	Thr	Phe	Val	Glu	Asn	Arg	Phe	Tyr	Arg		
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cct	ctc	gga	ttg	cgg	cat	act	ttg	ttt	aat	ccg	ctc	caa	aag	ggc	ttt		1301
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gtt act atc att gat ccc gtg tat caa atc ggc att gtg ttg tta acc Val Thr Ile Ile Asp Pro Val Tyr Gln Ile Gly Ile Val Leu Leu Thr 395 400 405	1733
aat aaa aag cac tct cct gtt atc aac cct aaa gaa aac ccg aat caa Asn Lys Lys His Ser Pro Val Ile Asn Pro Lys Glu Asn Pro Asn Gln 410 415 420	1781
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<211> 448

<212> PRT

<213> Bacillus licheniformis

<400> 24

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Phe Ser Ser Lys Lys Leu Lys Ala Val Asp Arg Leu Ile Glu Gln Asp
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Val Lys Ala Gly Phe Pro Gly Ala Ala Leu Ile Leu Ile Lys Asp Gly
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Lys Ile Ile Lys Lys Glu Val Tyr Gly Tyr Lys Gln Lys Tyr Asn Gly
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Leu Ile Ala Leu Lys His Pro Lys Lys Met Lys Ala Asn Thr Met Phe
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Asp Leu Ala Ser Asn Thr Lys Met Tyr Ala Val Asn Phe Ala Leu Gln
 115 120 125

His Leu Val Ser Thr Gly Lys Leu Asp Leu Asn Lys Asn Ile Ser Gln
 130 135 140

Tyr Leu Pro Asp Phe Lys Asp His Pro Glu Asp Asp Val Lys Gly Lys
 145 150 155 160

Asn Arg Leu Arg Val Ile Asp Leu Leu His His Asn Ala Gly Phe Pro
 165 170 175

Ala Ser Trp Asn Tyr Tyr Asp Pro Lys Ser Ala Gly His Leu Tyr Ser
 180 185 190

Gln Ser Arg Ser Lys Thr Leu Glu Tyr Leu Val Lys Thr Pro Leu Ala
 195 200 205

Tyr Glu Pro Gly Thr Lys Gln Ile Tyr Ser Asp Ile Asp Tyr Met Leu
 210 215 220

Leu Gly Leu Ile Ile Glu Lys Ile Thr Asn Glu Arg Leu Asp Thr Phe
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Val Glu Asn Arg Phe Tyr Arg Pro Leu Gly Leu Arg His Thr Leu Phe
 245 250 255
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 260 265 270
 Arg Leu Gly Asn Thr Arg Asp Gly Thr Ile Ser Phe Pro Asn Ile Arg
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 Thr Tyr Thr Leu Gln Gly Glu Val His Asp Glu Lys Ala Phe Tyr Ser
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 Met Glu Gly Val Ser Gly His Ala Gly Leu Phe Ser Thr Val Asp Asp
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 Lys Thr Asn Pro Thr Tyr Gly Leu Gly Trp Arg Leu Asn Gly Asn Thr
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 385 390 395 400
 Ile Gly Ile Val Leu Leu Thr Asn Lys Lys His Ser Pro Val Ile Asn
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<211> 3060

<212> DNA

<213> Bacillus licheniformis

<220>

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atg Met	ggg Gly	aaa Lys	atc Ile 220	gcc Ala	gat Asp	atg Met	ctt Leu	gaa Glu 225	tct Ser	gcc Ala	ggg Gly	aat Asn	acg Thr 230	gcg Ala	acc Thr	1084
ccg Pro	ctg Leu	caa Gln 235	aga Arg	agg Arg	ctt Leu	gaa Glu 240	gag Glu 240	ctc Leu	ggc Gly	aaa Lys	att Ile	ttg Leu 245	att Ile	gtc Val	gcc Ala	1132
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cat His 265	gat Asp	tta Leu	tac Tyr	agc Ser	atg Met 270	ttt Phe	tta Leu	gcg Ala	gga Gly	gtt Val 275	tcc Ser	ctt Leu	gcc Ala	gtc Val	gct Ala 280	1228
gcc Ala	ata Ile	cct Pro	gaa Glu 285	ggg Gly 285	ctg Leu	cct Pro	gcc Ala	att Ile	gtc Val 290	acg Thr	gtc Val	gct Ala	ctg Leu	tct Ser 295	ctc Leu	1276
ggc Gly	gtg Val	cag Gln	cgg Arg 300	atg Met	atc Ile	agg Arg	caa Gln	aag Lys 305	tcg Ser	atc Ile	gtc Val	agg Arg	aag Lys 310	ctg Leu	ccc Pro	1324
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ggg Gly 330	acg Thr	atg Met	acg Thr	cag Gln	aac Asn	aaa Lys 335	atg Met	acg Thr	gtc Val	acc Thr	cat His 340	gtc Val	tgg Trp	tca Ser	ggc Gly	1420
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10294.000.ST25.txt

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Ser	Ala	Ala	Leu	Glu	Thr	Leu	Ala	Ser	Gln	Ala	Leu	Arg	Thr	Ile	Ala		
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Val	Ala	Tyr	Lys	Pro	Ile	Lys	Asp	Thr	Glu	Asn	Pro	Pro	Leu	Glu	Lys		
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Ala	Glu	Ser	Gly	Leu	Thr	Phe	Ile	Gly	Leu	Leu	Gly	Met	Ile	Asp	Pro		
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Asp	Gly	Val	Asn	Asp	Ala	Pro	Ala	Ile	Lys	Gln	Ala	Asp	Ile	Gly	Ile		
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Ile	Leu	Val	Asp	Asp	Asn	Phe	Ala	Thr	Ile	Lys	Ser	Ala	Ile	Lys	Glu		
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gga	cgc	aat	atc	tat	gaa	aat	att	aga	aag	ttc	atc	aga	tac	ttg	ctc	2476	
Gly	Arg	Asn	Ile	Tyr	Glu	Asn	Ile	Arg	Lys	Phe	Ile	Arg	Tyr	Leu	Leu		
				685					690					695			
gca	tcc	aat	gtc	ggc	gaa	att	ttg	gtc	atg	ctg	ttt	gca	atg	ctg	ctc	2524	
Ala	Ser	Asn	Val	Gly	Glu	Ile	Leu	Val	Met	Leu	Phe	Ala	Met	Leu	Leu		
			700					705					710				
gct	ctg	ccg	ctg	ccg	ctt	gtc	ccg	ata	cag	att	ctg	tgg	gtc	aac	ctt	2572	
Ala	Leu	Pro	Leu	Pro	Leu	Val	Pro	Ile	Gln	Ile	Leu	Trp	Val	Asn	Leu		
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10294.000.ST25.txt

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 Asp Asp Val Met Gln Arg Lys Pro Arg Ser Pro Lys Glu Gly Val Phe
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 gca agg ggg ctc ggc tgg aag gtc gta tcg cgc gga ttc tta atc gga 2716
 Ala Arg Gly Leu Gly Trp Lys Val Val Ser Arg Gly Phe Leu Ile Gly
 765 770 775
 atc gcg aca ctc ggg gcg ttt atg ttc att tat aac cgc aat cca gaa 2764
 Ile Ala Thr Leu Gly Ala Phe Met Phe Ile Tyr Asn Arg Asn Pro Glu
 780 785 790
 gcg ctt gag tat gca cag acg gtt gca ttt gca acg ctc gtc ctt gcg 2812
 Ala Leu Glu Tyr Ala Gln Thr Val Ala Phe Ala Thr Leu Val Leu Ala
 795 800 805
 cag ctg atc cac gtg ttc gac tgc cga agc gag cgg tcc atc ttt gac 2860
 Gln Leu Ile His Val Phe Asp Cys Arg Ser Glu Arg Ser Ile Phe Asp
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 Arg Asn Pro Phe Glu Asn Ile Tyr Leu Leu Gly Ala Val Leu Ser Ser
 825 830 835 840
 att ctt ttg atg ctt gtc gtt att tat tat ccg ccg ctg cag ccg att 2956
 Ile Leu Leu Met Leu Val Val Ile Tyr Tyr Pro Pro Leu Gln Pro Ile
 845 850 855
 ttt cat acg gtt ccg att tta atg gca gac tgg ctc ctg att gtc gga 3004
 Phe His Thr Val Pro Ile Leu Met Ala Asp Trp Leu Leu Ile Val Gly
 860 865 870
 atg tcg gcg att cca act ttt tta ctg gcc ggg tca ctt tta caa gaa 3052
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 Lys Asn
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<211> 890

<212> PRT

<213> Bacillus licheniformis

<400> 26

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Val Ala Leu Phe Phe Ser Gln Phe Lys Asp Phe Met Val Leu Val Leu
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 Ile Ala Ile Ile Ala Ile Ile Phe Val Asn Gly Ile Leu Gly Phe Phe
 85 90 95
 Gln Glu Arg Arg Ala Glu Arg Ser Leu Glu Ala Leu Lys Glu Leu Ser
 100 105 110
 Ala Pro Gln Val Ala Val Leu Arg Glu Gly Asn Trp Val Lys Ile Pro
 115 120 125
 Ser Lys Glu Leu Val Pro Gly Asp Val Val Arg Phe Ala Ser Gly Asp
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 Arg Ile Gly Ala Asp Leu Arg Leu Val Glu Thr Lys Ser Leu Glu Ile
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 Glu Glu Ser Ala Leu Thr Gly Glu Ser Leu Pro Val Ser Lys Gln Ala
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 Asp Ala Phe Gln Ala Ser Asp Val Ser Leu Gly Asp Leu Lys Asn Met
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 Ile Gly Thr Gly Met Asn Ser Ala Met Gly Lys Ile Ala Asp Met Leu
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 225 230 235 240
 Leu Gly Lys Ile Leu Ile Val Ala Ala Leu Phe Leu Thr Leu Leu Val
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 Ala Gly Val Ser Leu Ala Val Ala Ala Ile Pro Glu Gly Leu Pro Ala
 275 280 285
 Ile Val Thr Val Ala Leu Ser Leu Gly Val Gln Arg Met Ile Arg Gln
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 Lys Ser Ile Val Arg Lys Leu Pro Ala Val Glu Thr Leu Gly Cys Ala
 305 310 315 320

Ser Ile Ile Cys Ser Asp Lys Thr Gly Thr Met Thr Gln Asn Lys Met
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 Thr Val Thr His Val Trp Ser Gly Gly Lys Ile Trp Asn Val Ser Gly
 340 345 350
 Ile Gly Tyr Glu Pro Glu Gly Ser Phe Ser Met Asn Gly Arg Asp Val
 355 360 365
 Gln Ala Lys His His Lys Pro Leu Gln Gln Val Leu Leu Phe Gly Ala
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 Leu Cys Asn Ser Ser Ser Ile Ile Glu Lys Asp Gly Glu Phe Arg Leu
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 Asp Gly Asp Pro Thr Glu Gly Ala Leu Leu Thr Ala Ala Arg Lys Ala
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 Gly Phe Thr Asp Lys Tyr Val Asp Glu His Phe Lys Ile Ile Glu Glu
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 Lys Ser Gly Lys Arg Phe Val Ile Thr Lys Gly Ala Pro Asp Val Leu
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 Met Lys Arg Ser Ser His Thr Leu Thr Glu Glu Lys Arg Glu Ile Phe
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 485 490 495
 Ser Gln Ala Leu Arg Thr Ile Ala Val Ala Tyr Lys Pro Ile Lys Asp
 500 505 510
 Thr Glu Asn Pro Pro Leu Glu Lys Ala Glu Ser Gly Leu Thr Phe Ile
 515 520 525
 Gly Leu Leu Gly Met Ile Asp Pro Pro Arg Pro Glu Val Lys Thr Ala
 530 535 540
 Ile Lys Glu Cys Arg Glu Ala Gly Ile Lys Thr Val Met Ile Thr Gly
 545 550 555 560
 Asp His Val Ile Thr Ala Thr Ala Ile Ala Lys Asp Leu Gly Leu Leu
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 Pro Pro Arg Gly Lys Val Met Asp Gly Gln Met Leu Asn Glu Leu Ser
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Gln Glu Glu Leu Ala Glu Ile Val Asp Asp Val Tyr Val Phe Ala Arg
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Val Ser Pro Glu His Lys Leu Lys Ile Val Thr Ala Tyr Gln Glu Asn
610 615 620

Gly His Ile Val Ala Met Thr Gly Asp Gly Val Asn Asp Ala Pro Ala
625 630 635 640

Ile Lys Gln Ala Asp Ile Gly Ile Ser Met Gly Ile Thr Gly Thr Asp
645 650 655

Val Ala Lys Glu Ala Ser Ser Leu Ile Leu Val Asp Asp Asn Phe Ala
660 665 670

Thr Ile Lys Ser Ala Ile Lys Glu Gly Arg Asn Ile Tyr Glu Asn Ile
675 680 685

Arg Lys Phe Ile Arg Tyr Leu Leu Ala Ser Asn Val Gly Glu Ile Leu
690 695 700

Val Met Leu Phe Ala Met Leu Leu Ala Leu Pro Leu Pro Leu Val Pro
705 710 715 720

Ile Gln Ile Leu Trp Val Asn Leu Val Thr Asp Gly Leu Pro Ala Met
725 730 735

Ala Leu Gly Met Asp Gln Pro Glu Asp Asp Val Met Gln Arg Lys Pro
740 745 750

Arg Ser Pro Lys Glu Gly Val Phe Ala Arg Gly Leu Gly Trp Lys Val
755 760 765

Val Ser Arg Gly Phe Leu Ile Gly Ile Ala Thr Leu Gly Ala Phe Met
770 775 780

Phe Ile Tyr Asn Arg Asn Pro Glu Ala Leu Glu Tyr Ala Gln Thr Val
785 790 795 800

Ala Phe Ala Thr Leu Val Leu Ala Gln Leu Ile His Val Phe Asp Cys
805 810 815

Arg Ser Glu Arg Ser Ile Phe Asp Arg Asn Pro Phe Glu Asn Ile Tyr
820 825 830

Leu Leu Gly Ala Val Leu Ser Ser Ile Leu Leu Met Leu Val Val Ile
835 840 845

Tyr Tyr Pro Pro Leu Gln Pro Ile Phe His Thr Val Pro Ile Leu Met
850 855 860

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<220>

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<222> (501)..(3122)

<223>

<400> 27

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tcaagcaact gcttgaggaa agccatttca gagacatcac ggtacatatg aacaaaaatt	300
actgctgcat ttctgcggta aaatcatgaa ctttgtatga tcatcccttt caatacggaa	360
gggatttttt atgttttgata gagttgaaac tggatcttaa atatcatatt tttgattttt	420
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tatatatttcc ggagggtattt atg aac aaa agg atc gtg aaa agt tca att gtt	533
Met Asn Lys Arg Ile Val Lys Ser Ser Ile Val	
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ttc ttt ctc ctt gcc gca tta att ttt ggc cag ctg cct tta ccg aag	581
Phe Phe Leu Leu Ala Ala Leu Ile Phe Gly Gln Leu Pro Leu Pro Lys	
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Thr Met Ala Ala Glu Asp Ser Val Pro Asn Asn Glu Thr Thr Leu Thr	
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agc gcg tcc cct gtt gaa gct tcg ttt caa agc gat gac gag gtg cat	677
Ser Ala Ser Pro Val Glu Ala Ser Phe Gln Ser Asp Asp Glu Val His	
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Trp Tyr Lys Val Asn Pro Ser Asn Gln Glu Ile Ala Asn Tyr Thr His	
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ggc Gly	tac Tyr	tcc Ser 110	tat Tyr	gaa Glu	aat Asn	aat Asn	cct Pro 115	gct Ala	tta Leu	atc Ile	gat Asp	ttt Phe 120	ccg Pro	att Ile	gcc Ala	869
tgg Trp	aaa Lys 125	ggt Gly	cct Pro	tac Tyr	tac Tyr	ata Ile 130	aaa Lys	gta Val	gaa Glu	aat Asn	cac His 135	cat His	gat Asp	gag Glu	gaa Glu	917
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ccc Pro	ctc Leu	ggt Gly 350	aaa Lys	agc Ser	aaa Lys	acg Thr	gca Ala 355	ttt Phe	aaa Lys	gat Asp	atg Met	tac Tyr 360	gtt Val	gtg Val	gaa Glu	1589

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ccg Pro 620	gga Gly	acc Thr	gat Asp	att Ile	cca Pro 625	agc Ser	ctc Leu	gtt Val	ccg Pro 630	gac Asp	ggg Gly	aat Asn	gtc Val	act Thr	tat Tyr 635	2405

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gcc agc gtt ttt gag ctg aac atg aag gtt cat ccc gtt tta aac cgc Ala Ser Val Phe Glu Leu Asn Met Lys Val His Pro Val Leu Asn Arg 720 725 730	2693
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<400> 28

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 Pro Ser Asn Gln Glu Ile Ala Asn Tyr Thr His Phe Arg Val Lys Leu
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 Lys Ser Asp Ala Glu Leu Asn Ile Ser Val Tyr Ser Ser Leu Glu Asn
 85 90 95
 Ala Thr Gly His Gln Thr Phe Asp Arg Tyr Asn Gly Tyr Ser Tyr Glu
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 Asn Asn Pro Ala Leu Ile Asp Phe Pro Ile Ala Trp Lys Gly Pro Tyr
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 Ile Thr Asp Ile Ser Tyr Thr Ile Ser Tyr Glu Gly Val Thr Leu Pro
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 Pro Ser Ile Gln Glu Ala Glu Glu Glu Cys Pro Ala Glu Leu Ser Val
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 Lys Ser Met Arg Asp Ser Val Tyr Lys Asp Leu Val Gln Leu Lys Pro
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 Ser Ser Gly Phe Lys Ala Ala Ala Lys Gln Tyr Gln Ala Ala Ala Ser
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 385 390 395 400
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 Ser Val Lys Lys Asp Glu Gly Tyr Asn Tyr Val Gly Arg Thr Ala Asp
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 Glu Gln Ile Ala Asn Gly Ile Ile Tyr Ala Ala Asp His Gly Ala Lys
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 Val Ile Asn Leu Ser Leu Gly Gly Pro Tyr Ser Arg Val Met Glu Tyr
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 Ala Leu Lys Tyr Ala Ala Ser Lys Asn Val Thr Ile Val Ala Ala Thr
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 Gly Asn Asp Gly Val Ser Glu Ile Ser Tyr Pro Ala Ser Ser Lys Tyr
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 Thr Leu Ser Val Gly Ala Thr Asn Asn Leu Asp Leu Val Ser Asp Tyr
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 Ser Asn Tyr Gly Lys Gly Leu Asp Met Val Ala Pro Gly Thr Asp Ile
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 Pro Ser Leu Val Pro Asp Gly Asn Val Thr Tyr Met Ser Gly Thr Ser
 625 630 635 640
 Met Ala Ala Pro His Val Ala Ala Ala Ala Gly Leu Leu Leu Ser Gln
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 Asn Pro Ser Leu Lys Pro Lys Gln Ile Ala Ser Leu Leu Thr Glu Thr
 660 665 670
 Thr Ala Asp Val Ala Phe Glu Glu Gln Asp Asn Pro Asn Pro Asp Tyr
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 Asp Leu Asp Ile Glu Pro Ala Ala Gln Ile Pro Gly Tyr Asp Phe Val
 690 695 700
 Ser Gly Trp Gly Arg Leu Asn Val Phe His Ala Ala Ser Val Phe Glu
 705 710 715 720

Leu Asn Met Lys Val His Pro Val Leu Asn Arg His Thr Ala Val Thr
725 730 735

Gly Thr Ala Lys Ser Gly Val Thr Val Lys Ile Leu Arg Gly Lys Gln
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Val Leu Gly Thr Gly Thr Ala Gly Lys Ser Gly Ala Phe Ser Val Lys
755 760 765

Ile Pro Ala Gln Lys Ala Gly Gln Val Leu His Val Ala Ala Ser Gly
770 775 780

His Gln Ala Glu Thr Ser Leu Arg Thr Val Val Glu Lys Ala Pro Lys
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Asn Pro Ser Val Lys Arg Ile Thr Asn Lys Asp Thr Ala Val Thr Gly
805 810 815

Arg Thr Ala Ala Gly Tyr Thr Ile Lys Val Lys Asn Ala Tyr Lys Lys
820 825 830

Val Ile Ala Gln Gly Ile Ala Asp Ala Ser Val Ser Val Lys Val Lys
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<211> 2185

<212> DNA

<213> Bacillus licheniformis

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<222> (490)..(1686)

<223>

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aaaacatgac atggatgatg ccgctttttt tatctttaag cagtttcttt tggccgaaca 180

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 cctttcattt ccccaacctt aaatccccctt gaactacctt tatcttaaat aatgaatgag 420
 tgttcagtca atatattttc ataaatgcag gaaaataggg ggacactatt ctttacacga 480
 aaaaaggga gtg tct tca ttg gtg ccg ctt atg att atg gta tgt ttt ctc 531
 Val Ser Ser Leu Val Pro Leu Met Ile Met Val Cys Phe Leu
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 atc ctg ctt ctt gcg ctc gat ttc cat ttt ggc cgc aaa gcc ttt gag 579
 Ile Leu Leu Leu Ala Leu Asp Phe His Phe Gly Arg Lys Ala Phe Glu
 15 20 25 30
 aag aaa gcc tac gag ccc gtt ttt tca gag aag aaa agc gat att gaa 627
 Lys Lys Ala Tyr Glu Pro Val Phe Ser Glu Lys Lys Ser Asp Ile Glu
 35 40 45
 ctg att cat aat gga gaa gac ttg tgt gag cgg ctg ctg gat gac atc 675
 Leu Ile His Asn Gly Glu Asp Leu Cys Glu Arg Leu Leu Asp Asp Ile
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 Arg Gln Ala Glu Ser Ser Val His Val Met Phe Tyr Ile Val Lys Asn
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 Asp Asp Ile Ser Leu Glu Phe Leu Lys Val Leu Lys Asp Lys Ala Lys
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 Ser Gly Val Cys Val Arg Leu Leu Ile Asp Arg Ile Gly Ala Met Lys
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 Val Lys Lys Lys Thr Leu Ser Gly Leu Lys Gln Ser Gly Val His Val
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 Ala Asp Leu Gln His Ile Phe Ile Ser Asp Phe Lys Arg Glu Ala Pro
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 210 215 220
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 Val Thr His Thr Thr His Ala Thr Lys Gly Phe Ser Leu Glu Glu Lys
 225 230 235

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Lys	Ala	Leu	Ile	Val	Asp	Asp	Arg	His	Val	Met	Ile	Gly	Thr	Ser	Asn		
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Phe	Asp	Asn	Arg	Ser	Leu	Phe	Leu	Asn	Asp	Glu	Val	Asn	Val	Val	Ile		
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His	Asp	Lys	Asp	Trp	Thr	Lys	Gln	Phe	Phe	Asp	Val	Val	Lys	Glu	Ser		
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Ile	Glu	His	Ala	Glu	Leu	Leu	Thr	Lys	Glu	Arg	Tyr	Ala	Lys	Arg	Pro		
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Val	Met	Gln	Arg	Pro	Val	Glu	Trp	Leu	Ala	Lys	Ser	Ile	Ser	Phe	Phe		
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Leu																	
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<213> Bacillus licheniformis

<400> 30

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 His Asn Gly Glu Asp Leu Cys Glu Arg Leu Leu Asp Asp Ile Arg Gln
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 Ala Glu Ser Ser Val His Val Met Phe Tyr Ile Val Lys Asn Asp Asp
 65 70 75 80
 Ile Ser Leu Glu Phe Leu Lys Val Leu Lys Asp Lys Ala Lys Ser Gly
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 Val Cys Val Arg Leu Leu Ile Asp Arg Ile Gly Ala Met Lys Val Lys
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 Lys Lys Thr Leu Ser Gly Leu Lys Gln Ser Gly Val His Val Phe Phe
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 Ala Asn Lys Pro Gly Phe Pro Tyr Phe Phe Tyr Arg Leu Asn Ala Arg
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 Asn His Arg Lys Ile Ala Val Ile Asp Gly Lys Ile Gly Tyr Val Gly
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 Pro Trp Lys Asp Tyr His Leu Arg Met Thr Gly Glu Gly Val Ala Asp
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 Leu Gln His Ile Phe Ile Ser Asp Phe Lys Arg Glu Ala Pro Gln Ala
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 Lys Pro Ala Asn Ser Val Phe Pro Pro Leu Gln Gln Gly Ala Val Thr
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 His Thr Thr His Ala Thr Lys Gly Phe Ser Leu Glu Glu Lys Tyr Ile
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 Ser Phe Ile Glu Gln Ala Lys Glu Arg Ile Met Ile Cys Thr Pro Tyr
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290 295 300
Gly Cys Tyr Ile Tyr Arg Tyr Tyr Arg Gly Phe Tyr His Ala Lys Ala
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Leu Ile Val Asp Asp Arg His Val Met Ile Gly Thr Ser Asn Phe Asp
325 330 335
Asn Arg Ser Leu Phe Leu Asn Asp Glu Val Asn Val Val Ile His Asp
340 345 350
Lys Asp Trp Thr Lys Gln Phe Phe Asp Val Val Lys Glu Ser Ile Glu
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<213> Bacillus licheniformis

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<222> (124)..(2058)

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aag gaa ttg tgg aca ttg atc gaa cta ttt agt gat tat gtg ctc cat 168
Glu Leu Trp Thr Leu Ile Glu Leu Phe Ser Asp Tyr Val Leu His
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ttt gaa cgt tat ttt gtt tta agc aga cag agc atg ctt gtc att cag 216

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Pro	Phe	Met	Gln	Phe	Leu	Leu	Phe	Gly	Tyr	Ile	Leu	Leu	Val	Ser	Phe		
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Cys	Leu	Phe	Phe	Gln	Leu	Tyr	Trp	Lys	Arg	Asn	Arg	Tyr	Val	Leu	Leu		
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Leu	Asn	Pro	Phe	Tyr	Asn	Leu	Ala	Asp	Ala	Ala	Phe	Thr	Ile	Ser	His		
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acc	aat	tat	cac	aat	caa	aaa	aag	cct	agc	ggg	aat	atc	ctg	tcc	ggc	1176
Thr	Asn	Tyr	His	Asn	Gln	Lys	Lys	Pro	Ser	Gly	Asn	Ile	Leu	Ser	Gly	
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Gln	Ala	Tyr	Ile	Lys	Arg	Ser	Lys	Gln	Phe	Leu	Arg	Glu	His	Gly	Arg	
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Glu	Lys	Asp	Leu	Ile	Glu	Phe	Gln	Lys	Lys	Glu	Ser	Asp	Ala	Val	Leu	
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ttaccagact	gtcctcattt	taagagagtt	tcaagagctg	tcatacgagg	aatagcgga											2748
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gaaaaaaagc	ttggaaggca	gggaggttta	acaatatgaa	atgccatctt	gtaagagatt											2868
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<210> 32

<211> 645

<212> PRT

<213> Bacillus licheniformis

<400> 32

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 20 25 30
 Cys Val Thr Gly Leu Val Leu Leu Tyr Ala Val Ser Phe His Pro Lys
 35 40 45
 Val Cys Arg Arg Arg Leu Phe Phe Tyr Ala Gly Ile Val Leu Arg Leu
 50 55 60
 Ile Leu Val Gly Ala Leu Ser Phe Glu Leu Ala His Gln Met Lys Ala
 65 70 75 80
 Ala Glu Phe Ser Asn Leu Tyr Ile Asp Glu Gln Asp Ala Leu Leu Pro
 85 90 95
 Phe Met Gln Phe Leu Leu Phe Gly Tyr Ile Leu Leu Val Ser Phe His
 100 105 110
 Tyr Met Met Thr Leu Ala Glu Lys Gly Gly Lys Gly Leu Phe Phe Ala
 115 120 125
 Phe Asp Ile Ala Val Met Ala Met Pro Leu Phe Gln Ser Leu Phe Ser
 130 135 140
 Phe Ala Ala Tyr Leu Lys Glu Phe Gly Ala Glu Glu Leu Glu Glu Leu
 145 150 155 160
 Pro Leu Val Leu Leu Leu Ile Val Gly Ile Pro Gly Leu Met Ile Cys
 165 170 175
 Leu Phe Phe Gln Leu Tyr Trp Lys Arg Asn Arg Tyr Val Leu Leu Leu
 180 185 190
 Ile Phe Tyr Ile Val Thr Ile Gly Gly Phe Phe Ile Lys Lys Leu Gly
 195 200 205
 Tyr Glu Phe Phe Pro Leu Asn Val Phe Leu Thr Met Ile Gly Phe Leu
 210 215 220
 Met Thr Tyr His Leu Leu Asn Asp Ser Arg Lys Pro Leu Leu Met Val
 225 230 235 240
 Lys Arg Val Leu Ala Ala Gly Thr Ala Val Phe Phe Thr Leu His Leu
 245 250 255
 Asn Pro Phe Tyr Asn Leu Ala Asp Ala Ala Phe Thr Ile Ser His Pro
 260 265 270
 Glu Val Ser Asp Val Val Asp Ala Asn Phe Arg Pro Val Ser Val Lys
 275 280 285

Glu Ala Lys Gln Thr Val Ser Ser Phe Phe Pro Thr Glu Ser Phe Ile
 290 295 300
 Tyr Leu Ser Ala Thr Asn Gln Asp Phe His Asn Val Tyr His Phe Lys
 305 310 315 320
 Thr Lys Asp Tyr Asp Ala Asp Val Asp Gly Trp Thr Gly Met Ile Thr
 325 330 335
 Asn Tyr His Asn Gln Lys Lys Pro Ser Gly Asn Ile Leu Ser Gly Gln
 340 345 350
 Ala Tyr Ile Lys Arg Ser Lys Gln Phe Leu Arg Glu His Gly Arg Glu
 355 360 365
 Leu Asp Lys Gln Ile Lys Ala Lys Val Ser Arg Asp Asp Gly Glu Ala
 370 375 380
 Thr Val Glu Phe Tyr Arg Glu Gly Glu Asp Pro Glu Leu Ser Thr Met
 385 390 395 400
 Trp Phe Thr Trp Arg Lys Glu Thr Leu Met Gly Phe His Glu Asp Ala
 405 410 415
 Ser Val Tyr Ser Leu Glu Ser Val Asn Gln Ala Arg Val Ser Gly Glu
 420 425 430
 Asp Ile Glu Arg Gly Val Glu Ala Val Tyr Arg Lys Leu Gly Ile Pro
 435 440 445
 Val Ser Ser Tyr Arg Leu Thr Asp Ile Asp Leu Leu Phe Pro Phe Ser
 450 455 460
 Leu Asn Ser Ala Ser Ile Asn Ile Lys Thr Ser Asp Gly Met Gly Met
 465 470 475 480
 Glu Phe His Pro Val Thr Gly Ala Leu Thr Ala Ile Ser Ile Lys Ser
 485 490 495
 Glu Ser Ala Leu Pro Tyr Arg Gly Gln Glu Leu Glu Lys Arg Leu Leu
 500 505 510
 Ser Leu Phe Asp Gln Asp Ile Ser Asn Leu Lys Arg Val Glu Leu Glu
 515 520 525
 Lys Asp Leu Ile Glu Phe Gln Lys Lys Glu Ser Asp Ala Val Leu Asn
 530 535 540
 Thr Val Trp Thr Met Thr Lys His Glu Glu Gly Ala Tyr Leu Thr Val
 545 550 555 560

10294.000.ST25.txt

Arg Lys Asn Phe Gln Lys Ala Asp Glu Lys Pro Pro Tyr Thr Tyr Ala
565 570 575

Asp Gly Glu Lys Ala Phe Gln Lys Val Ser Glu Arg Tyr Gln Lys Gly
580 585 590

Leu Val Tyr His Lys Arg Thr Lys Leu Val Ile Val Ser Asp Gly Asp
595 600 605

Gln Lys Ser Arg Tyr Ala Trp Leu Val Ile Ile Gln Pro Phe Gly Ser
610 615 620

Asn Glu His Asp Ala Tyr Leu Val Asp Ala Glu Thr Asp Glu Val Lys
625 630 635 640

His Phe Asp Asp Lys
645

<210> 33

<211> 1712

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1211)

<223>

<400> 33
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ttatatgacg gctgcatcga ctttgccatt gaggcataatt tgctgggagc cgagtacggg 180
aagttcggct atcacggaga acccgttcat cgagcgaatga tccgctcaga aaaagaagaa 240
aaacagctac tgcacgagct ttatgaatat gctgtcagct ggtctgaggc ttttaatggt 300
caagctgctt atgaaccgct ctattatgcc tgcgaatact tcatccaaag ctggtggaag 360
gaaggcttca gccagcggga aagacgcttt aagcttcggc tcagataaaa caaagtttta 420
tgaaaaagtg aggccaagct taatcatatt tcctttcctt gtcccatatc ttgtagtaag 480
gacgagcggg agggaaaggg atg aag aaa aaa ata aaa tgg ctc ggg ttt tta 533
Met Lys Lys Lys Ile Lys Trp Leu Gly Phe Leu
1 5 10
ctc ggc ttt gtc gtt tta tta tgt tta ttt caa tat caa ttc aac aat 581
Leu Gly Phe Val Val Leu Leu Cys Leu Phe Gln Tyr Gln Phe Asn Asn
15 20 25

gat gat tct tgg cgg tca tgg aat ctt ccg ctg agc ggc aaa atc att Asp Asp Ser Trp Arg Ser Trp Asn Leu Pro Leu Ser Gly Lys Ile Ile 30 35 40	629
tat att gat cct gga cac ggg ggc gcc gat gga ggg gca tca agc ggt Tyr Ile Asp Pro Gly His Gly Gly Ala Asp Gly Gly Ala Ser Ser Gly 45 50 55	677
gaa ctc ctt gaa aaa gac gtg gct ctt gaa gta tcc cta aga atc agg Glu Leu Leu Glu Lys Asp Val Ala Leu Glu Val Ser Leu Arg Ile Arg 60 65 70 75	725
gac tat ctc cag gag cag ggc gcc ttg gtg atg ctg acg cgg gag gac Asp Tyr Leu Gln Glu Gln Gly Ala Leu Val Met Leu Thr Arg Glu Asp 80 85 90	773
gat cat gat ctc gct cct gaa gaa acg agg gga ctc agc aga aga aaa Asp His Asp Leu Ala Pro Glu Glu Thr Arg Gly Leu Ser Arg Arg Lys 95 100 105	821
gct gaa gac ttg cgg aag agg gtc gat atg atc aac aat tct gaa gcc Ala Glu Asp Leu Arg Lys Arg Val Asp Met Ile Asn Asn Ser Glu Ala 110 115 120	869
gat ctt tac ctc agc atc cat ttg aat gcg att cct tcc gcg cga tgg Asp Leu Tyr Leu Ser Ile His Leu Asn Ala Ile Pro Ser Ala Arg Trp 125 130 135	917
agc ggt gcg caa agc ttc tat tac ggg caa tat gaa gag aat gaa cgg Ser Gly Ala Gln Ser Phe Tyr Tyr Gly Gln Tyr Glu Glu Asn Glu Arg 140 145 150 155	965
gcc gcc aag ttt att cag gat gaa tta aga cat aat ctt gaa aac acg Ala Ala Lys Phe Ile Gln Asp Glu Leu Arg His Asn Leu Glu Asn Thr 160 165 170	1013
acg cgg aag gca aag cgg ata cac gga att tat ttg atg caa aat gtt Thr Arg Lys Ala Lys Arg Ile His Gly Ile Tyr Leu Met Gln Asn Val 175 180 185	1061
aaa aag ccc ggg gcc ctt gtc gaa atc ggg ttt ttg tct aac ccg gaa Lys Lys Pro Gly Ala Leu Val Glu Ile Gly Phe Leu Ser Asn Pro Glu 190 195 200	1109
gag gca aaa cag ctg gcc aag ccc aaa tat cag gac aaa atc gca gca Glu Ala Lys Gln Leu Ala Lys Pro Lys Tyr Gln Asp Lys Ile Ala Ala 205 210 215	1157
tcc gtt tat aaa ggc gta ttg cgc tac ttt aca gaa gac aga gac cct Ser Val Tyr Lys Gly Val Leu Arg Tyr Phe Thr Glu Asp Arg Asp Pro 220 225 230 235	1205
cct gaa taagagggtt tctttttgtg tcaaagacac tataaggaaa gatatgctat Pro Glu	1261
acttatttttg taaacgaata caacaaaggg tgagatcaat gttgcgagaa gacgatgtaa	1321
aaaagatagt cggcgatttg gacgagccat ttcttcacaa gccgctcaga gagctggatg	1381
ccgtaaaaga aattaaata aaacccgaaa aacggcacgt cagcgtaaag gtggcgctcg	1441
caaaaacggg atctgccgaa caaatgcagc ttcagcagga aatcgtcata cggttgaaag	1501
aagccggtgc agagacgggc ggcctgcgtt ttgaggagct gcccgaagaa gtcgtaatga	1561
gttatcaaga gtctgccaaa gggcaggatc aatctctgct gaatagtga aaacagcctg	1621

10294.000.ST25.txt

tgttttttagc tgtggcaagc ggcaaaggcg gcgtcggcaa gtcgacggtg tcggtcaatt 1681
tggctgtgtc cctggcgcgga atcggaaaga a 1712

<210> 34

<211> 237

<212> PRT

<213> Bacillus licheniformis

<400> 34

Met Lys Lys Lys Ile Lys Trp Leu Gly Phe Leu Leu Gly Phe Val Val
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Leu Leu Cys Leu Phe Gln Tyr Gln Phe Asn Asn Asp Asp Ser Trp Arg
20 25 30
Ser Trp Asn Leu Pro Leu Ser Gly Lys Ile Ile Tyr Ile Asp Pro Gly
35 40 45
His Gly Gly Ala Asp Gly Gly Ala Ser Ser Gly Glu Leu Leu Glu Lys
50 55 60
Asp Val Ala Leu Glu Val Ser Leu Arg Ile Arg Asp Tyr Leu Gln Glu
65 70 75 80
Gln Gly Ala Leu Val Met Leu Thr Arg Glu Asp Asp His Asp Leu Ala
85 90 95
Pro Glu Glu Thr Arg Gly Leu Ser Arg Arg Lys Ala Glu Asp Leu Arg
100 105 110
Lys Arg Val Asp Met Ile Asn Asn Ser Glu Ala Asp Leu Tyr Leu Ser
115 120 125
Ile His Leu Asn Ala Ile Pro Ser Ala Arg Trp Ser Gly Ala Gln Ser
130 135 140
Phe Tyr Tyr Gly Gln Tyr Glu Glu Asn Glu Arg Ala Ala Lys Phe Ile
145 150 155 160
Gln Asp Glu Leu Arg His Asn Leu Glu Asn Thr Thr Arg Lys Ala Lys
165 170 175
Arg Ile His Gly Ile Tyr Leu Met Gln Asn Val Lys Lys Pro Gly Ala
180 185 190
Leu Val Glu Ile Gly Phe Leu Ser Asn Pro Glu Glu Ala Lys Gln Leu
195 200 205

Ala Lys Pro Lys Tyr Gln Asp Lys Ile Ala Ala Ser Val Tyr Lys Gly
210 215 220

Val Leu Arg Tyr Phe Thr Glu Asp Arg Asp Pro Pro Glu
225 230 235

<210> 35

<211> 1988

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1487)

<223>

<400> 35

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aagaatctag	ttagagcgggtg	gagcagggga	ttccttatta	tgactgcgat	tttgcacatt	180
tctccatttt	cctgcaaggt	caaaagacat	agttcttaag	ttttggattt	ttggtgtgtt	240
tattttttgt	ttcacaaact	ttaaggtaat	tttaagaaag	aggcgatctt	gccaaccccta	300
aacagggttt	ttcgaacaga	atgtcaaata	gattagatat	ttcataagaa	caaggggggaa	360
ttgtctgttt	gtgatgaata	aaggaggacg	ggcggaattt	ctgtcaggat	gctcagctgg	420
gttccttagaa	aaaaatgcgg	ctaaatatat	atttatagat	tgtaaacgct	gtcttgtcct	480
cgaccaacag	ggggatgaag	atg aag aag ctg tta gtt gtt tat gcc gtg atg				533
		Met Lys Lys Leu Leu Val Val Tyr Ala Val Met				
		1 5 10				

ctc tgt ttg ttt ttt ctg tat gtc tac gac tac tcc cgg ggc gat aaa 581
Leu Cys Leu Phe Phe Leu Tyr Val Tyr Asp Tyr Ser Arg Gly Asp Lys
15 20 25

gcc ggt tct gca gaa gaa agc agg agg cct gcg gcc gca ggc agt ctg 629
Ala Gly Ser Ala Glu Glu Ser Arg Arg Pro Ala Ala Ala Gly Ser Leu
30 35 40

tcc gaa aaa tac gtg atg gtc acg ttt caa tcg gga atc gaa tat tgg 677
Ser Glu Lys Tyr Val Met Val Thr Phe Gln Ser Gly Ile Glu Tyr Trp
45 50 55

aag agc ggt ctg aaa ggc ttt gag gat gcc gcg cag ctt ttc aac gtc 725
Lys Ser Gly Leu Lys Gly Phe Glu Asp Ala Ala Gln Leu Phe Asn Val
60 65 70 75

tct gtc gag tat cgg ggg gcg gcc cat tat gat gtc cat gag caa acg 773

10294.000.ST25.txt

ser val glu tyr arg gly ala ala his tyr asp val his glu gln thr
 80 85 90
 acc gtc ctc gag cag gtg att gca aaa aaa ccg gcg gga atc gct gtt 821
 thr val leu glu gln val ile ala lys lys pro ala gly ile ala val
 95 100 105
 tcg gca ata aac cca aaa gct tta aac cct gtc atc gac aag gcg cac 869
 ser ala ile asn pro lys ala leu asn pro val ile asp lys ala his
 110 115 120
 gag cag ggt att ccg atc gtt tta ttt gat tca gac gcc ccg ctc agc 917
 glu gln gly ile pro ile val leu phe asp ser asp ala pro leu ser
 125 130 135
 aaa gct tct aca tat atc ggc aca aat aat atg gaa gcg ggt gct gtg 965
 lys ala ser thr tyr ile gly thr asn asn met glu ala gly ala val
 140 145 150 155
 gcc gca agg cga atg gcc gaa ttt ttg aat gga aag gga gaa acc gcg 1013
 ala ala arg arg met ala glu phe leu asn gly lys gly glu thr ala
 160 165 170
 gtc att acc cag ccg cag cag tac aat cat cag gaa agg acg aag ggc 1061
 val ile thr gln pro gln gln tyr asn his gln glu arg thr lys gly
 175 180 185
 ttt gaa caa acg atc aag caa aaa tac ccg aac atg aag gtt gcc gcg 1109
 phe glu gln thr ile lys gln lys tyr pro asn met lys val ala ala
 190 195 200
 gtt ttg gac gga aaa ggg gat gag ctg acg tcg aaa aaa gaa gcg gcg 1157
 val leu asp gly lys gly asp glu leu thr ser lys lys glu ala ala
 205 210 215
 aag att ttg gag gaa aat ccg tcc atc aaa gga att ttc acg act gaa 1205
 lys ile leu glu glu asn pro ser ile lys gly ile phe thr thr glu
 220 225 230 235
 gcc aat gga gcg agc ggc gtg gcc cgt gct gtg aag gag gcg gga ctt 1253
 ala asn gly ala ser gly val ala arg ala val lys glu ala gly leu
 240 245 250
 gaa ggg gaa gta tgt atc atc ggc ttt gat aaa gac aag aaa acg ctg 1301
 glu gly glu val cys ile ile gly phe asp lys asp lys lys thr leu
 255 260 265
 gac ggc atc aaa aac gga tcg att tcc gcg aca atg agc cag gac aca 1349
 asp gly ile lys asn gly ser ile ser ala thr met ser gln asp thr
 270 275 280
 tgg caa atg ggc tat tgg tcg ctg cac atg ctg ttt ttc tca aat cac 1397
 trp gln met gly tyr trp ser leu his met leu phe phe ser asn his
 285 290 295
 cat ctg aag cat gaa cgc ccg ctt ccg gcc gca atc gac aca ggc att 1445
 his leu lys his glu arg pro leu pro ala ala ile asp thr gly ile
 300 305 310 315
 acc atc ata acg aaa gaa aat gtg gca gcc tat tat gcg aat 1487
 thr ile ile thr lys glu asn val ala ala tyr tyr ala asn
 320 325
 gattaaacgt ttgatcaata atgcgccgat ccgtcataag ctgatcagcc ttctcttggt 1547
 aatcagcatg ctgccgacga tcggcctggg cattttatcg ggatgggccg ttgaaaatat 1607
 tattgaaaaa caggtgatcg accaaacact gcagctgacg ggcgaagtga acaagacggc 1667

10294.000.ST25.txt

tgaagtgtat gtcagccaca tgcagaacct gacatatatta atatcaatga atgaagaaat 1727
 ggaagcggtt tttagtcata aaaaggagga tggagaggcg gattataagc gaaggacgtt 1787
 tttgcagggc ctgacttctt tatattccga agcagcgggt attctcgttg tcaatgataa 1847
 ggggtgagatg atcagcaatg agatgtatga acgcacgccg acagatttga caaaagaacc 1907
 atggtatcag gcggctctcg acaatgaagg gattttcaag atgatcgggg agcctgtcaa 1967
 ccggaatatc agaagccatg t 1988

<210> 36

<211> 329

<212> PRT

<213> Bacillus licheniformis

<400> 36

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 20 25 30

Glu Ser Arg Arg Pro Ala Ala Ala Gly Ser Leu Ser Glu Lys Tyr Val
 35 40 45

Met Val Thr Phe Gln Ser Gly Ile Glu Tyr Trp Lys Ser Gly Leu Lys
 50 55 60

Gly Phe Glu Asp Ala Ala Gln Leu Phe Asn Val Ser Val Glu Tyr Arg
 65 70 75 80

Gly Ala Ala His Tyr Asp Val His Glu Gln Thr Thr Val Leu Glu Gln
 85 90 95

Val Ile Ala Lys Lys Pro Ala Gly Ile Ala Val Ser Ala Ile Asn Pro
 100 105 110

Lys Ala Leu Asn Pro Val Ile Asp Lys Ala His Glu Gln Gly Ile Pro
 115 120 125

Ile Val Leu Phe Asp Ser Asp Ala Pro Leu Ser Lys Ala Ser Thr Tyr
 130 135 140

Ile Gly Thr Asn Asn Met Glu Ala Gly Ala Val Ala Ala Arg Arg Met
 145 150 155 160

Ala Glu Phe Leu Asn Gly Lys Gly Glu Thr Ala Val Ile Thr Gln Pro
 165 170 175

10294.000.ST25.txt

Gln Gln Tyr Asn His Gln Glu Arg Thr Lys Gly Phe Glu Gln Thr Ile
180 185 190
Lys Gln Lys Tyr Pro Asn Met Lys Val Ala Ala Val Leu Asp Gly Lys
195 200 205
Gly Asp Glu Leu Thr Ser Lys Lys Glu Ala Ala Lys Ile Leu Glu Glu
210 215 220
Asn Pro Ser Ile Lys Gly Ile Phe Thr Thr Glu Ala Asn Gly Ala Ser
225 230 235 240
Gly Val Ala Arg Ala Val Lys Glu Ala Gly Leu Glu Gly Glu Val Cys
245 250 255
Ile Ile Gly Phe Asp Lys Asp Lys Lys Thr Leu Asp Gly Ile Lys Asn
260 265 270
Gly Ser Ile Ser Ala Thr Met Ser Gln Asp Thr Trp Gln Met Gly Tyr
275 280 285
Trp Ser Leu His Met Leu Phe Phe Ser Asn His His Leu Lys His Glu
290 295 300
Arg Pro Leu Pro Ala Ala Ile Asp Thr Gly Ile Thr Ile Ile Thr Lys
305 310 315 320
Glu Asn Val Ala Ala Tyr Tyr Ala Asn
325

<210> 37

<211> 2785

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(2282)

<223>

<400> 37

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acagtgattt aaacaagatg ttcggctctc cagatgcacc ggcagaagcg cagaatctga 180

10294.000.ST25.txt

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aaatgttaaa	ttcggcctct	tctcacactt	ggcaccctct	tactcataag	acatcgatct	360
gaaaattccc	aaaatataaa	caaaacatta	ataaaatcaa	gccatttgat	taacaaattt	420
acgatacgat	catatagaac	ttgatgattg	ggaaaagcat	tttgagagaa	gattaagagc	480
aaggggagata	tgatgtgaga	atg aaa cga tta agg atg agg aag cat tta ctg				533
		Met Lys Arg Leu Arg Met Arg Lys His Leu Leu				
		1 5 10				
ata gct gtc tgt act ttg gca ctt ctt cta agt tcc ccg att gta agc						581
Ile Ala Val Cys Thr Leu Ala Leu Leu Leu Ser Ser Pro Ile Val Ser						
		15 20 25				
gat gcg agc ccg gca act aaa cca aca act gca gat tcg ccg caa tct						629
Asp Ala Ser Pro Ala Thr Lys Pro Thr Thr Ala Asp Ser Pro Gln Ser						
		30 35 40				
tcc gga ttt ttc gta gac cat tac aaa aat aat atc tct gcc aat acg						677
Ser Gly Phe Phe Val Asp His Tyr Lys Asn Asn Ile Ser Ala Asn Thr						
		45 50 55				
acg gcg gaa tcc aat cct gtc atc ggc ctg ctt tcc gaa ttt aat aaa						725
Thr Ala Glu Ser Asn Pro Val Ile Gly Leu Leu Ser Glu Phe Asn Lys						
		60 65 70 75				
ctt tgg act ccc gga aag aca tgg aat acc ggt act aaa ctg aac agc						773
Leu Trp Thr Pro Gly Lys Thr Trp Asn Thr Gly Thr Lys Leu Asn Ser						
		80 85 90				
agg gtg ctg gat gcc aac att caa aaa gtc gtg gat att gct gaa cgc						821
Arg Val Leu Asp Ala Asn Ile Gln Lys Val Val Asp Ile Ala Glu Arg						
		95 100 105				
cgc acg atg ctt gag gaa aat gct gcc tat ttt gat gat cgg cgg agc						869
Arg Thr Met Leu Glu Glu Asn Ala Ala Tyr Phe Asp Asp Arg Arg Ser						
		110 115 120				
cag agc tac agt ata att gac ggc ctc ggc aag ctt gcc ggc gtc tat						917
Gln Ser Tyr Ser Ile Ile Asp Gly Leu Gly Lys Leu Ala Gly Val Tyr						
		125 130 135				
cga atg aac gcg gga gcg acg aca acg atc acc agc att ccg gca gat						965
Arg Met Asn Ala Gly Ala Thr Thr Thr Ile Thr Ser Ile Pro Ala Asp						
		140 145 150 155				
gcc tcg att aga aaa tac aat gat gaa gga acc aat tcg ggc agc acc						1013
Ala Ser Ile Arg Lys Tyr Asn Asp Glu Gly Thr Asn Ser Gly Ser Thr						
		160 165 170				
agc tct gaa ctt gga aat gtc gta agt ttg gtc aat act tta cgc ggc						1061
Ser Ser Glu Leu Gly Asn Val Val Ser Leu Val Asn Thr Leu Arg Gly						
		175 180 185				
aac tat tct tca tcg aat ccg gct aaa agc tat ttc aac tat ccc cgc						1109
Asn Tyr Ser Ser Ser Asn Pro Ala Lys Ser Tyr Phe Asn Tyr Pro Arg						
		190 195 200				
ccg ttt cgc tgg aaa gac aat tcg atc att gtt cca acg ctt atc ccc						1157
Pro Phe Arg Trp Lys Asp Asn Ser Ile Ile Val Pro Thr Leu Ile Pro						
		205 210 215				
gtc atc aat cct gat ccg aac aaa gac gga ggt ttt cca agc gga cac						1205

10294.000.ST25.txt

Val 220	Ile	Asn	Pro	Asp 225	Pro	Asn	Lys	Asp	Gly 230	Gly	Phe	Pro	Ser	Gly	His 235	
acg Thr	aac Asn	gcc Ala	gca Ala	tat Tyr 240	ctc Leu	agc Ser	gct Ala	ttt Phe	gct Ala 245	atg Met	gcc Ala	tat Tyr	gcg Ala	ata Ile 250	ccg Pro	1253
gag Glu	cgt Arg	tat Tyr	cag Gln 255	gag Glu	ctg Leu	ctg Leu	act Thr	cgc Arg 260	gct Ala	tca Ser	gaa Glu	ctc Leu	ggg Gly 265	cat His	aac Asn	1301
cgg Arg	att Ile	gtt Val 270	gcc Ala	ggg Gly	atg Met	cat His	tcc Ser 275	ccg Pro	ctg Leu	gac Asp	gtc Val	atg Met 280	ggg Gly	gga Gly	cga Arg	1349
gta Val 285	atg Met	gca Ala	aca Thr	gct Ala	ttg Leu	tct Ser 290	gca Ala	gca Ala	atc Ile	ctg Leu	tct Ser 295	gac Asp	ccc Pro	gca Ala	aat Asn	1397
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10294.000.ST25.txt

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Lys Ile Lys Gly Lys Ala Arg Leu Lys Gly Thr Leu Arg Leu Asn Phe
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Val Glu Gln Lys Gly Arg Ser
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<213> Bacillus licheniformis

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35 40 45

10294.000.ST25.txt

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 Lys Thr Trp Asn Thr Gly Thr Lys Leu Asn Ser Arg Val Leu Asp Ala
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 Ile Asp Gly Leu Gly Lys Leu Ala Gly Val Tyr Arg Met Asn Ala Gly
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 Asn Val Val Ser Leu Val Asn Thr Leu Arg Gly Asn Tyr Ser Ser Ser
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 195 200 205
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 210 215 220
 Pro Asn Lys Asp Gly Gly Phe Pro Ser Gly His Thr Asn Ala Ala Tyr
 225 230 235 240
 Leu Ser Ala Phe Ala Met Ala Tyr Ala Ile Pro Glu Arg Tyr Gln Glu
 245 250 255
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 405 410 415
 Thr Val Thr Met Asp Ser Ala Lys Gly Gly Phe His Thr Ala Asp Arg
 420 425 430
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 Gly Ala Leu Lys Leu Glu Gly Asp Asn Thr Tyr Ser Gly Gly Thr Arg
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 Ile Asp Gln Gly Thr Leu Glu Gly Gly Ser Glu Thr Ala Phe Gly Arg
 465 470 475 480
 Gly Asp Val Ala Leu Asn Gly Gly Ile Leu Lys Glu Asp Ala Pro Gly
 485 490 495
 Lys Leu Ile Ile Glu Gly Asp Tyr Lys Gln Ser Ala Lys Gly Ile Leu
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 Ala Arg Leu Lys Gly Thr Leu Arg Leu Asn Phe Thr Asp Asn Tyr Val
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 Pro Ala Asp Gly Ser Ala Ile Ile Thr Phe Arg Lys Arg His Gly Ser
 545 550 555 560
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<211> 2009

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<213> *Bacillus licheniformis*

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<222> (501)..(1526)

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gtttgaacag gaagcagcag tgcctcctct gttcatgttc atgggaaaac ataacattta      480
catttttgga gggtattttt ttg aag gtc ttt ctt aaa gct gta cct atg ttg      533
                        1  Leu Lys Val Phe 5  Leu Lys Ala Val 10  Pro Met Leu

tcg tta cgg ttc ttt ttg ttt gtg cct aat gta ttt gcg gcc aac tct      581
Ser Leu Arg Phe Phe Leu Phe Val 20  Pro Asn Val Phe Ala 25  Ala Asn Ser

gtc aca aga ttg gac ggt gca aac cga tat gag gtt gcg gtg aac gtt      629
Val Thr Arg 30  Leu Asp Gly Ala 35  Asn Arg Tyr Glu Val 40  Ala Val Asn Val

tcc aag cag ggg tgg aca agt gca agc act gtg att gtt gca aat gga      677
Ser Lys 45  Gln Gly Trp Thr 50  Ser Ala Ser Thr Val 55  Ile Val Ala Asn Gly

aag gca tat gca gac gtc ctt tca gcg act cca ttt gcc tat cga aac      725
Lys Ala Tyr Ala Asp Val 65  Leu Ser Ala Thr 70  Pro Phe Ala Tyr Arg Asn 75

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Asn Ala Pro Val 80  Leu Leu Thr Glu Ala 85  Ser Lys Leu Pro Thr 90  Ala Thr

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gcg aga aac ggc atc ccg att ctt tta aca tcg tcg aat tcc ata ccg Ala Arg Asn Gly Ile Pro Ile Leu Leu Thr Ser Ser Asn Ser Ile Pro 175 180 185	1061
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gct tct ccg acg cgg atc ggc ggc agc aac cgc tat gaa gtc gcg gcc Ala Ser Pro Thr Arg Ile Gly Gly Ser Asn Arg Tyr Glu Val Ala Ala 220 225 230 235	1205
aat gtc gtc aag aaa tat tat tct tct gcc aag aat gca atc atc agc Asn Val Val Lys Lys Tyr Tyr Ser Ser Ala Lys Asn Ala Ile Ile Ser 240 245 250	1253
aac ggc tat gcg tat gcc gac gga tta aca gga tct gtt ctg gcg gct Asn Gly Tyr Ala Tyr Ala Asp Gly Leu Thr Gly Ser Val Leu Ala Ala 255 260 265	1301
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<212> PRT

<213> Bacillus licheniformis

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35 40 45

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Val Leu Ser Ala Thr Pro Phe Ala Tyr Arg Asn Asn Ala Pro Val Leu
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Leu Thr Glu Ala Ser Lys Leu Pro Thr Ala Thr Lys Asn Arg Ile Ser
85 90 95

Gln Leu Lys Pro Ser Lys Val Ile Val Ile Gly Gly Thr Val Ser Val
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Gln Asn Gly Val Val Ser Glu Ile Lys Lys Leu Gly Val Ser Ser Val
115 120 125

Glu Arg Ile Gly Gly Ala Asn Arg Tyr Glu Val Ala Ala Asn Ile Ala
130 135 140

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145 150 155 160

Tyr Ala Asp Ser Leu Ala Ile Gly Ala Tyr Ala Ala Arg Asn Gly Ile
165 170 175

Pro Ile Leu Leu Thr Ser Ser Asn Ser Ile Pro Thr Ala Thr Lys Asn
180 185 190

Ala Met Lys Ser Lys Gly Thr Thr Ser Thr Ile Val Val Gly Gly Glu
 195 200 205

Val Ser Ile Ser Ser Ser Val Tyr Lys Gln Leu Ala Ser Pro Thr Arg
 210 215 220

Ile Gly Gly Ser Asn Arg Tyr Glu Val Ala Ala Asn Val Val Lys Lys
 225 230 235 240

Tyr Tyr Ser Ser Ala Lys Asn Ala Ile Ile Ser Asn Gly Tyr Ala Tyr
 245 250 255

Ala Asp Gly Leu Thr Gly Ser Val Leu Ala Ala Lys Gln Asn Arg Pro
 260 265 270

Met Met Phe Thr Asn Ala Ser Ser Leu Pro Thr Pro Thr Arg Glu Val
 275 280 285

Ile Gly Ser Lys Asn Met Thr Thr Phe Thr Val Leu Gly Gly Thr Val
 290 295 300

Ser Leu Gln Ser Asn Val Val Ser Gln Leu Lys Asn Pro Ile Val Gly
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<212> PRT

<213> Bacillus licheniformis

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 Lys Arg Leu Phe Val Pro Leu Arg Lys Lys Gly Glu Lys Gln Arg Thr
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65 70 75 80

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Val Tyr Gly Leu Ala Ala Gly His Ile Leu Leu Lys Arg Arg Arg Val
85 90 95

ctt gta cgt tct tgt cga tgt gga aaa aaa gcc gac ggt caa gct cat 815
Leu Val Arg Ser Cys Arg Cys Gly Lys Lys Ala Asp Gly Gln Ala His
100 105 110

tta tgt aaa aat gtc gga aat gat cag gga gtt aaa gct tcg ggt cga 863
Leu Cys Lys Asn Val Gly Asn Asp Gln Gly Val Lys Ala Ser Gly Arg
115 120 125

aat gta tca aga tca gca caa gta tcc gcc gta tca aaa agt cgt atc 911
Asn Val Ser Arg Ser Ala Gln Val Ser Ala Val Ser Lys Ser Arg Ile
130 135 140

caa gaa ctt att cat gct tta cca tta aaa gct cgg act gaa aga ggc 959
Gln Glu Leu Ile His Ala Leu Pro Leu Lys Ala Arg Thr Glu Arg Gly
145 150 155 160

gcc ttc tgt cac gag tcc gct ttc ggg cac ctc gct gcc gct tct cgt 1007
Ala Phe Cys His Glu Ser Ala Phe Gly His Leu Ala Ala Ala Ser Arg
165 170 175

cga tta aaa agg cga cat tca agt gga tta ccg gat gga ttt ggc caa 1055
Arg Leu Lys Arg Arg His Ser Ser Gly Leu Pro Asp Gly Phe Gly Gln
180 185 190

gct gat gaa gaa gtc gaa aaa aac ggt aaa gcc ggg cga gga agt cca 1103
Ala Asp Glu Glu Val Glu Lys Asn Gly Lys Ala Gly Arg Gly Ser Pro
195 200 205

aga ttt gat gtg gga aga gac gcc ttt cgt tcc ggc gtt ttc ggt aaa 1151
Arg Phe Asp Val Gly Arg Asp Ala Phe Arg Ser Gly Val Phe Gly Lys
210 215 220

gta cac agt gaa tta caa aca gga acc tgt ttt tct cga ata gaa tat 1199
Val His Ser Glu Leu Gln Thr Gly Thr Cys Phe Ser Arg Ile Glu Tyr
225 230 235 240

cgg tca aaa tgcaagtatc agtcatgaac ctttctcctc ggcataacaat 1248
Arg Ser Lys

gaggagaaag gttttttcat gtatgccgaa aaaatttccc taagctgtca tattgaaata 1308

ggacaacgtc atacactata gtgtcctggt tttgattgat gaagaagtaa aaaattgaaa 1368

aggattggaa gtccgggagg ggatcacttg gaaaaggctg atattttcaa ggatatcgct 1428

gaacgaacag gaggcgatat atacttaggt gtcgtaggag ctgtacgtac aggaaaatct 1488

acgtttatca aaaaatttat ggagctagtg gtgctcccga atatcaaaa tgaagcagac 1548

cgggcgcgcg cacaagatga gctcccccaa agtgccgctg gcaaaacat tatgacaacc 1608

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<210> 44

<211> 243

<212> PRT

<213> Bacillus licheniformis

<400> 44

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20 25 30Ala Ser Ala Pro Ala Gln Arg Ser Ala Gly Gly Arg Leu Leu Ile Gln
35 40 45Gly Gly Asp Gly Arg Ala Ser Ala Asp Ser Asp Lys Gly Tyr Gly Arg
50 55 60Ala Asn Leu Ser Lys Ile Pro Tyr Arg Phe Ser Gln Ala Val Pro Pro
65 70 75 80Val Tyr Gly Leu Ala Ala Gly His Ile Leu Leu Lys Arg Arg Arg Val
85 90 95Leu Val Arg Ser Cys Arg Cys Gly Lys Lys Ala Asp Gly Gln Ala His
100 105 110Leu Cys Lys Asn Val Gly Asn Asp Gln Gly Val Lys Ala Ser Gly Arg
115 120 125Asn Val Ser Arg Ser Ala Gln Val Ser Ala Val Ser Lys Ser Arg Ile
130 135 140Gln Glu Leu Ile His Ala Leu Pro Leu Lys Ala Arg Thr Glu Arg Gly
145 150 155 160Ala Phe Cys His Glu Ser Ala Phe Gly His Leu Ala Ala Ala Ser Arg
165 170 175Arg Leu Lys Arg Arg His Ser Ser Gly Leu Pro Asp Gly Phe Gly Gln
180 185 190Ala Asp Glu Glu Val Glu Lys Asn Gly Lys Ala Gly Arg Gly Ser Pro
195 200 205

10294.000.ST25.txt

Arg Phe Asp Val Gly Arg Asp Ala Phe Arg Ser Gly Val Phe Gly Lys
 210 215 220

Val His Ser Glu Leu Gln Thr Gly Thr Cys Phe Ser Arg Ile Glu Tyr
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Arg Ser Lys

<210> 45

<211> 1759

<212> DNA

<213> Bacillus Ticheniformis

<220>

<221> CDS

<222> (476)..(1267)

<223>

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 tgctctccgt ttaccgcttt ttctagatct ttgatcagcc tgttgttttg cctggcgggga 240
 taggcgggat gatacggctg aacataccac atgtttttca cctcaatata ttatatattg 300
 ccgtcctgtc attatatgta agtcgaagct tgcattgtgcc tactggaagg gcgcattctc 360
 gacatgtggc aaaatgggtg ggggagagcg caatctatit taaaaaatg aagtttgacg 420
 taaaatgggt gttagtgcgg aatgggtgaca tacatatcaa aatggagtga gacta ttg 478
 Leu
 1

aaa aag gca ata ttg acg gtc ata gct gta ttg acg tcg gtt gtt ttg 526
 Lys Lys Ala Ile Leu Thr Val Ile Ala Val Leu Thr Ser Val Val Leu
 5 10 15

ttc gcc ggc tgc caa gcg gaa aaa ggg gga tca gcc aag ggg cag tct 574
 Phe Ala Gly Cys Gln Ala Glu Lys Gly Gly Ser Ala Lys Gly Gln Ser
 20 25 30

gaa aaa gtt caa att acg gtt tcc gcg gct gcg agt ctc aag gat gtt 622
 Glu Lys Val Gln Ile Thr Val Ser Ala Ala Ala Ser Leu Lys Asp Val
 35 40 45

tta aca gaa ctt tcc tcc gtc tat gag aaa gac cat ccg aat gtc tct 670
 Leu Thr Glu Leu Ser Ser Val Tyr Glu Lys Asp His Pro Asn Val Ser
 50 55 60 65

ata aag ttt aat ttt ggt tca tcg ggt gca ttg cag cag cag atc gaa 718

10294.000.ST25.txt

Ile	Lys	Phe	Asn	Phe	Gly	Ser	Ser	Gly	Ala	Leu	Gln	Gln	Gln	Ile	Glu		
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Gln	Gly	Ala	Pro	Ala	Asp	Leu	Phe	Phe	Ser	Ala	Ala	Glu	Asp	Lys	Phe		
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aat	aga	gta	gtt	gat	caa	ggg	tta	att	gac	aaa	aaa	gac	tct	gtc	aag	814	
Asn	Arg	Val	Val	Asp	Gln	Gly	Leu	Ile	Asp	Lys	Lys	Asp	Ser	Val	Lys		
		100					105					110					
ctg	gtc	gaa	aac	agt	ctg	gtg	ctg	atc	gtg	ccg	aaa	gga	aaa	agt	cag	862	
Leu	Val	Glu	Asn	Ser	Leu	Val	Leu	Ile	Val	Pro	Lys	Gly	Lys	Ser	Gln		
	115					120					125						
cat	gtc	aac	agc	ttc	aag	gat	ttg	gcg	gat	gac	aaa	gtc	gaa	aaa	att	910	
His	Val	Asn	Ser	Phe	Lys	Asp	Leu	Ala	Asp	Asp	Lys	Val	Glu	Lys	Ile		
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Ala	Ile	Gly	Lys	Pro	Glu	Ser	Val	Pro	Ala	Gly	Lys	Tyr	Ala	Lys	Glu		
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Thr	Leu	Thr	Asn	Leu	Asp	Val	Trp	Ser	Lys	Val	Gln	Ser	Lys	Val	Val		
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tac	agc	aaa	gat	gta	agg	cag	gtc	ctt	tct	tat	atc	gaa	aca	ggc	aac	1054	
Tyr	Ser	Lys	Asp	Val	Arg	Gln	Val	Leu	Ser	Tyr	Ile	Glu	Thr	Gly	Asn		
		180					185					190					
gcg	gat	gcc	gga	atc	gtt	tac	cgg	acg	gac	gcc	ctt	tca	tca	gat	cag	1102	
Ala	Asp	Ala	Gly	Ile	Val	Tyr	Arg	Thr	Asp	Ala	Leu	Ser	Ser	Asp	Gln		
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gtc	gag	acc	gta	gag	acg	gcg	aaa	agc	gat	ctg	cat	aca	ccg	att	gtc	1150	
Val	Glu	Thr	Val	Glu	Thr	Ala	Lys	Ser	Asp	Leu	His	Thr	Pro	Ile	Val		
	210				215					220				225			
tat	ccg	ctc	gga	att	gtg	aaa	aat	aca	aag	cac	agg	gaa	cag	tct	gag	1198	
Tyr	Pro	Leu	Gly	Ile	Val	Lys	Asn	Thr	Lys	His	Arg	Glu	Gln	Ser	Glu		
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gaa	ttt	tat	caa	ttc	ctg	caa	agc	gac	caa	gcc	gtc	aag	gcg	atg	gaa	1246	
Glu	Phe	Tyr	Gln	Phe	Leu	Gln	Ser	Asp	Gln	Ala	Val	Lys	Ala	Met	Glu		
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Lys	Tyr	Gly	Phe	Lys	Lys	Gly											
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acggagcaaa	cgaatggagg	gtgttcctct	ttgtcaccgt	tccccttgca	tccaatggaa											1717	
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<211> 264

<212> PRT

<213> Bacillus licheniformis

<400> 46

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 20 25 30

Ser Glu Lys Val Gln Ile Thr Val Ser Ala Ala Ala Ser Leu Lys Asp
 35 40 45

Val Leu Thr Glu Leu Ser Ser Val Tyr Glu Lys Asp His Pro Asn Val
 50 55 60

Ser Ile Lys Phe Asn Phe Gly Ser Ser Gly Ala Leu Gln Gln Gln Ile
 65 70 75 80

Glu Gln Gly Ala Pro Ala Asp Leu Phe Phe Ser Ala Ala Glu Asp Lys
 85 90 95

Phe Asn Arg Val Val Asp Gln Gly Leu Ile Asp Lys Lys Asp Ser Val
 100 105 110

Lys Leu Val Glu Asn Ser Leu Val Leu Ile Val Pro Lys Gly Lys Ser
 115 120 125

Gln His Val Asn Ser Phe Lys Asp Leu Ala Asp Asp Lys Val Glu Lys
 130 135 140

Ile Ala Ile Gly Lys Pro Glu Ser Val Pro Ala Gly Lys Tyr Ala Lys
 145 150 155 160

Glu Thr Leu Thr Asn Leu Asp Val Trp Ser Lys Val Gln Ser Lys Val
 165 170 175

Val Tyr Ser Lys Asp Val Arg Gln Val Leu Ser Tyr Ile Glu Thr Gly
 180 185 190

Asn Ala Asp Ala Gly Ile Val Tyr Arg Thr Asp Ala Leu Ser Ser Asp
 195 200 205

Gln Val Glu Thr Val Glu Thr Ala Lys Ser Asp Leu His Thr Pro Ile
 210 215 220

Glu Glu Phe Tyr Gln Phe Leu Gln Ser Asp Gln Ala Val Lys Ala Met
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Glu Lys Tyr Gly Phe Lys Lys Gly
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<210> 47

<211> 2449

<212> DNA

<213> *Bacillus licheniformis*

<220>

<221> CDS

<222> (501) .. (1946)

<223>

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cac ggc tac aat ctt gtt ttc gcg ctg gcg ggc gat ccg aaa gac gtc His Gly Tyr Asn Leu Val Phe Ala Leu Ala Gly Asp Pro Lys Asp Val 110 115 120	869
gat gac aca tcc atc tat ttg ttc tat caa aag aaa ggc gaa act tct Asp Asp Thr Ser Ile Tyr Leu Phe Tyr Gln Lys Lys Gly Glu Thr Ser 125 130 135	917
atc gac agc tgg aaa aac gcc ggc aga gtg ttt aaa gac agc gac aaa Ile Asp Ser Trp Lys Asn Ala Gly Arg Val Phe Lys Asp Ser Asp Lys 140 145 150 155	965
ttt gtt cca gac gat ccg tac ctc aaa cat caa aca cag gaa tgg tca Phe Val Pro Asp Asp Pro Tyr Leu Lys His Gln Thr Gln Glu Trp Ser 160 165 170	1013
ggt tct gcc acg ctg aca aaa gac gga aaa gtc cga ctg ttt tac aca Gly Ser Ala Thr Leu Thr Lys Asp Gly Lys Val Arg Leu Phe Tyr Thr 175 180 185	1061
gct ttt tcc ggc acg caa tac ggc aag cag acg ctg aca aca gct cag Ala Phe Ser Gly Thr Gln Tyr Gly Lys Gln Thr Leu Thr Ala Gln 190 195 200	1109
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aac gtt cag caa ttc att gac gaa gga aac tac agc tcc ggc gac aac Asn Val Gln Gln Phe Ile Asp Glu Gly Asn Tyr Ser Ser Gly Asp Asn 240 245 250	1253
cat acg atg aga gac ccg cat tat gtg gaa gac cgc ggc cat aaa tat His Thr Met Arg Asp Pro His Tyr Val Glu Asp Arg Gly His Lys Tyr 255 260 265	1301
ctc gta ttt gaa gcc aat acg gga aca aaa acc ggc tac caa gga gaa Leu Val Phe Glu Ala Asn Thr Gly Thr Lys Thr Gly Tyr Gln Gly Glu 270 275 280	1349
gac tcc cta ttc aac aga gcc tac tac ggg ggc agc aag aag ttc ttt Asp Ser Leu Phe Asn Arg Ala Tyr Tyr Gly Gly Ser Lys Lys Phe Phe 285 290 295	1397
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tcg ctg gct aac ggc gct ctc gga atc atc gaa tta aat aac gat tat Ser Leu Ala Asn Gly Ala Leu Gly Ile Ile Glu Leu Asn Asn Asp Tyr 320 325 330	1493
aca ctg aaa aaa gtc atg aag cct ttg atc gcc tcc aat acg gtg aca Thr Leu Lys Lys Val Met Lys Pro Leu Ile Ala Ser Asn Thr Val Thr 335 340 345	1541

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gat gaa atc gaa cgg gcc aac ctc ttc aaa atg aat gga aaa tgg tat Asp Glu Ile Glu Arg Ala Asn Leu Phe Lys Met Asn Gly Lys Trp Tyr 350 355 360	1589
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tca aaa gac att tat atg ctc ggc tat gta tca ggt tca tta acc gga Ser Lys Asp Ile Tyr Met Leu Gly Tyr Val Ser Gly Ser Leu Thr Gly 380 385 390 395	1685
cca ttc aag cct tta aac aaa tcc gga ctt gtt ttg cat atg gac cag Pro Phe Lys Pro Leu Asn Lys Ser Gly Leu Val Leu His Met Asp Gln 400 405 410	1733
gat tac aat gac atc acg ttt act tat tca cac ttt gcc gta ccg cag Asp Tyr Asn Asp Ile Thr Phe Thr Tyr Ser His Phe Ala Val Pro Gln 415 420 425	1781
aaa aaa ggc gac gaa gtc gtc att aca agc tac atc aca aac aga ggg Lys Lys Gly Asp Glu Val Val Ile Thr Ser Tyr Ile Thr Asn Arg Gly 430 435 440	1829
att tcg aac gag cat cac gcc acg ttt gca cca agc ttt ttg ctg aag Ile Ser Asn Glu His His Ala Thr Phe Ala Pro Ser Phe Leu Leu Lys 445 450 455	1877
atc aaa gga tca aaa aca tcc gtt gtc aaa aac agc atc ctt gaa cag Ile Lys Gly Ser Lys Thr Val Ser Val Val Lys Asn Ser Ile Leu Glu Gln 460 465 470 475	1925
gga caa cta acg gta aac aaa taaaacgaac gaaggaaaat gccggtgaac Gly Gln Leu Thr Val Asn Lys 480	1976
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<210> 48

<211> 482

<212> PRT

<213> Bacillus licheniformis

<400> 48

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 Gln Asp Tyr₃₅ Lys Lys Ser Tyr Gly₄₀ Phe Ser His Ile Thr₄₅ Arg His Asp
 Met Leu₅₀ Lys Ile Pro Glu Gly₅₅ Gln Lys Ser Glu Gln₆₀ Phe Lys Val Pro
 Gln Phe Asp Pro Lys Thr₇₀ Ile Lys Asn Ile Pro₇₅ Ser Ala Lys Gly Tyr₈₀
 Asn Lys Asn Gly Glu₈₅ Leu Ile Asp Leu Asp₉₀ Val Trp Asp Ser Trp₉₅ Pro
 Leu Gln Asn Ala₁₀₀ Asp Gly Thr Val Ala₁₀₅ Thr Tyr His Gly Tyr₁₁₀ Asn Leu
 Val Phe Ala₁₁₅ Leu Ala Gly Asp Pro₁₂₀ Lys Asp Val Asp₁₂₅ Thr Ser Ile
 Tyr Leu₁₃₀ Phe Tyr Gln Lys Lys₁₃₅ Gly Glu Thr Ser Ile₁₄₀ Asp Ser Trp Lys
 Asn Ala Gly Arg Val Phe₁₅₀ Lys Asp Ser Asp Lys₁₅₅ Phe Val Pro Asp Asp₁₆₀
 Pro Tyr Leu Lys His₁₆₅ Gln Thr Gln Glu Trp₁₇₀ Ser Gly Ser Ala Thr₁₇₅ Leu
 Thr Lys Asp Gly₁₈₀ Lys Val Arg Leu Phe₁₈₅ Tyr Thr Ala Phe Ser₁₉₀ Gly Thr
 Gln Tyr Gly₁₉₅ Lys Gln Thr Leu Thr₂₀₀ Thr Ala Gln Val Asn₂₀₅ Phe Ser Gln
 Pro Asp₂₁₀ Ser Asp Thr Leu Lys₂₁₅ Ile Asp Gly Val Glu₂₂₀ Asp His Lys Ser
 Val Phe Asp Gly Ala Asp₂₃₀ Gly Thr Val Tyr Gln₂₃₅ Asn Val Gln Gln Phe₂₄₀
 Ile Asp Glu Gly Asn₂₄₅ Tyr Ser Ser Gly Asp₂₅₀ Asn His Thr Met Arg₂₅₅ Asp
 Pro His Tyr Val₂₆₀ Glu Asp Arg Gly His₂₆₅ Lys Tyr Leu Val Phe₂₇₀ Glu Ala
 Asn Thr Gly₂₇₅ Thr Lys Thr Gly Tyr₂₈₀ Gln Gly Glu Asp Ser₂₈₅ Leu Phe Asn

Arg Ala Tyr Tyr Gly Gly Ser Lys Lys Phe Phe Lys Glu Glu Ser Ser
 290 295 300

Lys Leu Leu Gln Gly Ala Asn Lys Lys Asn Ala Ser Leu Ala Asn Gly
 305 310 315 320

Ala Leu Gly Ile Ile Glu Leu Asn Asn Asp Tyr Thr Leu Lys Lys Val
 325 330 335

Met Lys Pro Leu Ile Ala Ser Asn Thr Val Thr Asp Glu Ile Glu Arg
 340 345 350

Ala Asn Leu Phe Lys Met Asn Gly Lys Trp Tyr Leu Phe Thr Asp Ser
 355 360 365

Arg Gly Ser Lys Met Thr Ile Asp Gly Ile Gly Ser Lys Asp Ile Tyr
 370 375 380

Met Leu Gly Tyr Val Ser Gly Ser Leu Thr Gly Pro Phe Lys Pro Leu
 385 390 395 400

Asn Lys Ser Gly Leu Val Leu His Met Asp Gln Asp Tyr Asn Asp Ile
 405 410 415

Thr Phe Thr Tyr Ser His Phe Ala Val Pro Gln Lys Lys Gly Asp Glu
 420 425 430

Val Val Ile Thr Ser Tyr Ile Thr Asn Arg Gly Ile Ser Asn Glu His
 435 440 445

His Ala Thr Phe Ala Pro Ser Phe Leu Leu Lys Ile Lys Gly Ser Lys
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Thr Ser Val Val Lys Asn Ser Ile Leu Glu Gln Gly Gln Leu Thr Val
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Asn Lys

<210> 49

<211> 1669

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<223>

[illegible]

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Gln Asp Ala Lys Gly Thr Ile Arg Ala Lys Asp Thr Gly Val Lys Tyr
195      200      205      1105

cag gta gcc att act tgg gtt gac gga aaa ggc tgg aag ccg aca aaa
Gln Val Ala Ile Thr Trp Val Asp Gly Lys Gly Trp Lys Pro Thr Lys
210      215      220      1153

gtt gaa caa ttg aaa taaagaaaaa agcggccggt tgctaaaacc gggcgctttt
Val Glu Gln Leu Lys
225      1208

tttatgattc ggctttaaaa tgaacgactg cgctgtagtg gatccgtccg tcaataaccg
1268

ccgtatggtg ggaaaccgaa tggaccctca gcaaaatcgc ctggttggtt tcaatctgct
1328

gactgatctt tttttcaagc tcctctaagc tcagtgcctc aaaaaactca attttatctt
1388

tgatcagatc gaggccgaag ttcataaacc aatcctccat tcggtttcaag tcatttttta
1448

ttaaagcaga gaagcggccg ggtgacaagg gaaatataac caagcctttt ttgtacccaa
1508

aacgaatgac ttgtggtagg ataagaacta atcaatcgaa taaatcatat tatacttata
1568

ggaattgtaa aaatagatgg agagtgcga caaaatggga agagagtcca ttcctttatt
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<210> 50

<211> 227

<212> PRT

<213> Bacillus licheniformis

<400> 50

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20      25      30

val val val Ala Ser Ser Leu Met Met Asn Ser Pro Lys Glu Gln Ala
35      40      45

Gln Gln Asp Val Ser Lys Asn Asp Ser Glu Gln Thr Thr Glu Ala Pro
50      55      60

Ala Ser Asp Asn Lys Lys Gln Thr Ser Asp Glu Asp Val Lys Asp Glu
65      70      75      80

Asp Lys Gly Lys Ser Asp Ser Ala Asp Lys Glu Asp Ser Asp Ser Asp
85      90      95

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Ser Asp Lys Asp Lys Glu Ser Ala Ser Asp Glu Asp Lys Ser Thr Ser
 100 105 110

Asp Asp Pro Phe Glu Gly Ala Glu Val Thr Glu Gly Gly Ser Ser Ala
 115 120 125

Asn Val Glu Lys Thr Ile Ile Asn Pro Asp Trp Glu Pro Val Gly Thr
 130 135 140

Gln Gln Ser Gly Gln His Thr Ala Thr Tyr Asp Ser Ser Ser Gln Asp
 145 150 155 160

Trp Lys Glu Met Leu Glu Ala Ile Ser Tyr Ala Thr Gly Val Ser Lys
 165 170 175

Asp Asn Met Thr Val Ile Trp Leu Gly Asn Asn Gly Ser Pro Gln Asp
 180 185 190

Ala Lys Gly Thr Ile Arg Ala Lys Asp Thr Gly Val Lys Tyr Gln Val
 195 200 205

Ala Ile Thr Trp Val Asp Gly Lys Gly Trp Lys Pro Thr Lys Val Glu
 210 215 220

Gln Leu Lys
 225

<210> 51

<211> 1700

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (437)..(1213)

<223>

<400> 51
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<213> Bacillus licheniformis

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Lys Ser Leu Phe Asp Arg Phe Thr Leu Lys Asp Arg Ala Ala Thr Gln
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<223>

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 100 105 110

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Ser	Asn	Ile	Cys	Leu	Lys	Ile	Gln	Arg	Gln	Ile	Arg	Arg	Tyr	Arg	Tyr	
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<213> Bacillus licheniformis

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Ile Met Asn Ala Thr Asp Gln Ala Leu Lys Asp Tyr Asp Leu Ser Lys
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Trp Thr Val Thr Ser Gly Ser Ser Ser Ala Met Thr Ala Ala Leu Lys
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Lys Ala Tyr Asp Lys Lys Asp Pro Ile Ile Ile Thr Gly Trp Thr Pro
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His Trp Met Phe Ala Lys Tyr Asp Leu Lys Tyr Leu Lys Asp Pro Lys
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Gly Ser Tyr Gly Asp Ala Glu Glu Ile His Thr Val Thr Arg Lys Gly
 115 120 125

Phe Lys Asp Asp His Pro Gly Ala Asn Lys Leu Leu Ser Gln Phe Ser
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Cys Phe Thr Cys Cys Met Ala Ala Ala Thr Gln Ser Asn Ile Cys Leu
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<222> (501)..(1181)

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 gccatcagca ttgccaagcg gacgaggacg attgtctggc agaataattat ttttgcactc 240
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Val Ile Asn Asn Gln Thr Gln Asn Ala Ser Gln Thr Phe Asp Asp Lys
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190 195 200
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Gly Val Lys Ile Asp Lys Pro Phe Asp Tyr Asp Lys Ile Lys Glu Thr
205 210 215
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<213> Bacillus licheniformis

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 Lys Phe His Glu Ala Leu Tyr Lys Ala Gln Pro Asp Asn Asp Thr Met
 130 135 140
 Glu Asn Glu Trp Ala Thr Pro Ala Lys Leu Ala Asp Ile Thr Glu Ala
 145 150 155 160
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Lys Val Phe Lys Gly Asp Ala Leu Tyr Glu Lys Asp Thr Ile Val Asn
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Asn Gln Lys Ser Val Ala Lys Ile Asp Val Val Ser Thr Tyr Asn Lys
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65 70 75 80

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Asp Asp Asn Asn Pro Leu Gly Tyr Glu Asp Tyr Lys Asp Pro Glu Tyr
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Ser Ile Glu Ala Tyr Leu Lys Ala Tyr Asp Pro Lys Lys Trp Gly Lys
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Lys Glu Pro Thr Gly Lys Leu Glu Glu Ala Arg Leu Arg Ser Lys Asp
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Lys Leu Lys
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<211> 1856

<212> DNA

<213> Bacillus licheniformis

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<222> (465)..(1358)

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ctg	cgc	aag	ctt	gat	gcc	ggc	agc	ttc	ttc	ggt	ccg	cag	ttc	gca	gga	860
Leu	Arg	Lys	Leu	Asp	Ala	Gly	Ser	Phe	Phe	Gly	Pro	Gln	Phe	Ala	Gly	
			120					125					130			
gag	cgc	att	ccg	aca	ttt	gaa	gaa	gtg	ctt	gac	cgg	tat	aaa	ggg	aag	908
Glu	Arg	Ile	Pro	Thr	Phe	Glu	Glu	Val	Leu	Asp	Arg	Tyr	Lys	Gly	Lys	
		135				140						145				
gtc	gga	atg	ctg	atc	gaa	ttg	aaa	gag	cct	gca	cgc	tat	ccg	gga	atc	956
Val	Gly	Met	Leu	Ile	Glu	Leu	Lys	Glu	Pro	Ala	Arg	Tyr	Pro	Gly	Ile	
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gaa	gga	aaa	gtg	tca	gca	gca	ttg	aaa	gag	cgg	aga	atg	gat	aag	cct	1004
Glu	Gly	Lys	Val	Ser	Ala	Ala	Leu	Lys	Glu	Arg	Arg	Met	Asp	Lys	Pro	
165					170					175					180	
aaa	aac	gga	aaa	atc	att	gta	caa	tcg	ttt	gat	ttt	aac	tct	gtc	tat	1052
Lys	Asn	Gly	Lys	Ile	Ile	Val	Gln	Ser	Phe	Asp	Phe	Asn	Ser	Val	Tyr	
				185					190					195		
aaa	att	cat	cag	ctg	ctt	cca	tcg	atg	ccg	aca	ggt	gtc	ttg	acg	tca	1100
Lys	Ile	His	Gln	Leu	Leu	Pro	Ser	Met	Pro	Thr	Gly	Val	Leu	Thr	Ser	
			200					205					210			
aaa	gcg	gcg	gac	tta	aca	gat	gca	aag	ctt	aag	gaa	ttt	tcc	ggc	tat	1148
Lys	Ala	Ala	Asp	Leu	Thr	Asp	Ala	Lys	Leu	Lys	Glu	Phe	Ser	Gly	Tyr	
		215					220					225				
gcc	aaa	tac	gtg	aac	gcc	aac	ttg	aaa	aat	gtg	gcc	gct	gat	cct	acg	1196
Ala	Lys	Tyr	Val	Asn	Ala	Asn	Leu	Lys	Asn	Val	Ala	Ala	Asp	Pro	Thr	
	230					235					240					
ctt	gtg	ccg	aga	att	cat	gcg	ctc	ggc	atg	aag	ata	cgc	cct	tgg	acc	1244
Leu	Val	Pro	Arg	Ile	His	Ala	Leu	Gly	Met	Lys	Ile	Arg	Pro	Trp	Thr	
245					250					255					260	
gtc	cgc	tcc	cgc	gat	gaa	gtg	cct	ccg	cta	tca	agg	ccc	gcg	tgg	aac	1292

10294.000.ST25.txt

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ggg att gtg aca aaa ctt tcc cga cta ttg ttc caa aaa agt acg gga      1340
Gly Ile Val Thr Lys Leu Ser Arg Leu Leu Phe Gln Lys Ser Thr Gly
      280      285      290
gcc cca ata aaa aac cct gaagtttgct ttgaagggt ttttaattta      1388
Ala Pro Ile Lys Asn Pro
      295
aaaaataaaaa tggggcttaa aacaaaaaag gttaacgtta acgggtttat cgttcccccc      1448
gattttttttt gggacacctg ggaaaaacgg gtataaacct ttggggggccc tttttggggg      1508
ccttaaaaaat tttgaaattt gccccggggg ccctccttgt ggccggaggg gggaaaattt      1568
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aaaaaaacccc ggggggttttt ttttttgggt actgccgccg atgaccttac atatgggctg      1688
aactgcaaaa acaatggaag aggaaaacct gcaggccgc atcgtctcat tcagcgttga      1748
tcccgaaaat gatacgctg aaaaattgaa gaaatttgcg gccaaactacc cgctcagttt      1808
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<211> 298

<212> PRT

<213> Bacillus licheniformis

<400> 64

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      20      25      30
Gly Ala Gln Glu Pro Ala Val Lys Pro Lys Lys Val Asp Val Ile Ala
      35      40      45
His Arg Gly Ala Ser Gly Tyr Ala Pro Glu Asn Thr Met Ala Ala Phe
      50      55      60
Asp Lys Ala Leu Gln Met Lys Ala Asp Tyr Ile Glu Leu Asp Val Gln
      65      70      75      80
Met Ser Lys Asp Gly Glu Leu Val Ile Ile His Asp Thr Thr Val Asn
      85      90      95
Arg Thr Thr Asp Ile Asp Ser Val Leu Pro Val Ala Val Lys Asp Leu
      100      105      110

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10294.000.ST25.txt

Thr Leu Ala Glu Leu Arg Lys Leu Asp Ala Gly Ser Phe Phe Gly Pro
115 120 125

Gln Phe Ala Gly Glu Arg Ile Pro Thr Phe Glu Glu Val Leu Asp Arg
130 135 140

Tyr Lys Gly Lys Val Gly Met Leu Ile Glu Leu Lys Glu Pro Ala Arg
145 150 155 160

Tyr Pro Gly Ile Glu Gly Lys Val Ser Ala Ala Leu Lys Glu Arg Arg
165 170 175

Met Asp Lys Pro Lys Asn Gly Lys Ile Ile Val Gln Ser Phe Asp Phe
180 185 190

Asn Ser Val Tyr Lys Ile His Gln Leu Leu Pro Ser Met Pro Thr Gly
195 200 205

Val Leu Thr Ser Lys Ala Ala Asp Leu Thr Asp Ala Lys Leu Lys Glu
210 215 220

Phe Ser Gly Tyr Ala Lys Tyr Val Asn Ala Asn Leu Lys Asn Val Ala
225 230 235 240

Ala Asp Pro Thr Leu Val Pro Arg Ile His Ala Leu Gly Met Lys Ile
245 250 255

Arg Pro Trp Thr Val Arg Ser Arg Asp Glu Val Pro Pro Leu Ser Arg
260 265 270

Pro Ala Trp Asn Gly Ile Val Thr Lys Leu Ser Arg Leu Leu Phe Gln
275 280 285

Lys Ser Thr Gly Ala Pro Ile Lys Asn Pro
290 295

<210> 65

<211> 1768

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1265)

<223>

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aacgatcaat tgatggacaa attggagcca tatccatatg atcagctgaa agatttttaaa 120
acggcctatt tggcaggcta catcgctgaa aaatataatt acgatgatga agagcttttt 180
ccgcggggcga aaagcaaaat cagcggctac atcgagtcac atatcgattc caccctgtcc 240
gggtacagct cagtcgatgt gaaaacgaaa cacgtcgata cacaaaaagt gaaaagcttg 300
tatgtgcttt tgcccgtctg gatgggtcaat tacaactaca aacaaaagga ttacatcttt 360
gccatgaacg gacaaacggg aaaagtcgtc ggcaagccgc cgatcagctc atttaaagaa 420
aaaatgtggt tcagcgggct ggccgtctcc atatttgcac tctggaaaat cattgctgct 480
gtaatgggag gcggggcgctg atg aga agt tta ttg aga agc gcg atg atc tta 533
Met Arg Ser Leu Leu Arg Ser Ala Met Ile Leu
1 5 10

tgt atg att ttc ctt gtc ttc atc cct ata gcc tcc ggt gcg gca gcc 581
Cys Met Ile Phe Leu Val Phe Ile Pro Ile Ala Ser Gly Ala Ala Ala
15 20 25

tct gaa cag aag cgg ttt gtt tat gat gaa gcc ggg ctt ctg acc aaa 629
Ser Glu Gln Lys Arg Phe Val Tyr Asp Glu Ala Gly Leu Leu Thr Lys
30 35 40

cag gaa atc gag aag ctg gaa acg ctg gca gcc aaa ttg ggc gcc gaa 677
Gln Glu Ile Glu Lys Leu Thr Leu Ala Ala Lys Leu Gly Ala Glu
45 50 55

cgg gag acc gac ttt atc att gtg acg acc aat gat aca aac ggc cgc 725
Arg Glu Thr Asp Phe Ile Val Thr Thr Asn Asp Thr Asn Gly Arg
60 65 70 75

gat gta aag aaa tat gcg gag gac ttc tat gac gaa aaa gcg ccc ggc 773
Asp Val Lys Lys Tyr Ala Glu Asp Phe Tyr Asp Glu Lys Ala Pro Gly
80 85 90

tac cag aag aag cac gga aat gca gcc gta tta acg gta gat atg gag 821
Tyr Gln Lys Lys His Gly Asn Ala Ala Val Leu Thr Val Asp Met Glu
95 100 105

cat aga gaa gtc tat ctt gcc ggc ttt aaa aag gct gaa gaa tat ttg 869
His Arg Glu Val Tyr Leu Ala Gly Phe Lys Lys Ala Glu Glu Tyr Leu
110 115 120

aat gac gcc agg ctg gac aaa att aga gaa aaa atc acg ccg gat ata 917
Asn Asp Ala Arg Leu Asp Lys Ile Arg Glu Lys Ile Thr Pro Asp Ile
125 130 135

tcc gac aag cat tat gag gcc gca ttc gaa atg ttt atg aag gcg gcg 965
Ser Asp Lys His Tyr Glu Ala Ala Phe Glu Met Phe Met Lys Ala Ala
140 145 150 155

cat gat gat atg gag aag aaa ccg tgg gcg gac agc atc ttt ttt aag 1013
His Asp Asp Met Glu Lys Lys Pro Trp Ala Asp Ser Ile Phe Phe Lys
160 165 170

acg tgg ttt caa ttg ctt gtt tcg gca gtc atc gcg gga att gcc gtc 1061
Thr Trp Phe Gln Leu Leu Val Ser Ala Val Ile Ala Gly Ile Ala Val
175 180 185

gcc att atg aaa tac aat tca ggc ggc aaa gtg aca gta agt gca agc 1109
Ala Ile Met Lys Tyr Asn Ser Gly Gly Lys Val Thr Val Ser Ala Ser
190 195 200

10294.000.ST25.txt

act tat atg aac ggt gat acg tcc gga gtg atc aga aat aat gac gaa 1157
 Thr Tyr Met Asn Gly Asp Thr Ser Gly Val Ile Arg Asn Asn Asp Glu
 205 210 215
 tac atc aga acg acc gtc aca aaa cag aga aaa ccg tcc aat aat aaa 1205
 Tyr Ile Arg Thr Thr Val Thr Lys Gln Arg Lys Pro Ser Asn Asn Lys
 220 225 230 235
 agc tca ggc ggc gga acg acg agc gga ggc cat tcg cac agc ggc agc 1253
 Ser Ser Gly Gly Gly Thr Thr Ser Gly Gly His Ser His Ser Gly Ser
 240 245 250
 cgg gga agc ttt tagaaaggga aaggaagagc ttaaattggtg ttttttagaa 1305
 Arg Gly Ser Phe
 255
 atcaatttgc aaatgtagta gagtgggatg aatttcgcga tgatatgatt ttctataaat 1365
 ggaacaaccg cgaaatcaaa aaggggagcc ggctgatcat tcgccccggt caggatgccg 1425
 tcttttttaa caacggaaaa attgaaggca ttttcaggga tgagggcgac tatgatattg 1485
 aatccgaaat tattcctttt ttatccactt taaaagggtt taaatttggc tttacagcg 1545
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 agaatgccat caatatcccc gctgcaggac ttccgggcgg catgccgatc agggcgaacg 1665
 gaagatttaa ctttaagggtg aatgattatg tcgcattaat cgataaaatt gccggtgtga 1725
 aagatcagta tgttgtggaa gatatcaaaa tacggatcac atc 1768

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<211> 255

<212> PRT

<213> Bacillus licheniformis

<400> 66

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 20 25 30
 Phe Val Tyr Asp Glu Ala Gly Leu Leu Thr Lys Gln Glu Ile Glu Lys
 35 40 45
 Leu Glu Thr Leu Ala Ala Lys Leu Gly Ala Glu Arg Glu Thr Asp Phe
 50 55 60
 Ile Ile Val Thr Thr Asn Asp Thr Asn Gly Arg Asp Val Lys Lys Tyr
 65 70 75 80
 Ala Glu Asp Phe Tyr Asp Glu Lys Ala Pro Gly Tyr Gln Lys Lys His
 85 90 95

10294.000.ST25.txt

Gly Asn Ala Ala Val Leu Thr Val Asp Met Glu His Arg Glu Val Tyr
100 105 110
Leu Ala Gly Phe Lys Lys Ala Glu Glu Tyr Leu Asn Asp Ala Arg Leu
115 120 125
Asp Lys Ile Arg Glu Lys Ile Thr Pro Asp Ile Ser Asp Lys His Tyr
130 135 140
Glu Ala Ala Phe Glu Met Phe Met Lys Ala Ala His Asp Asp Met Glu
145 150 155 160
Lys Lys Pro Trp Ala Asp Ser Ile Phe Phe Lys Thr Trp Phe Gln Leu
165 170 175
Leu Val Ser Ala Val Ile Ala Gly Ile Ala Val Ala Ile Met Lys Tyr
180 185 190
Asn Ser Gly Gly Lys Val Thr Val Ser Ala Ser Thr Tyr Met Asn Gly
195 200 205
Asp Thr Ser Gly Val Ile Arg Asn Asn Asp Glu Tyr Ile Arg Thr Thr
210 215 220
Val Thr Lys Gln Arg Lys Pro Ser Asn Asn Lys Ser Ser Gly Gly Gly
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<210> 67

<211> 2206

<212> DNA

<213> Bacillus licheniformis

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<223>

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gttcctaaatg ctgccttggt gtatgttttg gcgtgtgtgt agacggtatt aaaaaagtga 180

10294.000.ST25.txt

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ggagcgacag tcgtgcgtta agctggcagc tgacatcgta tgaattaaaa ggaatcttga 480
acaactgccg gccgaagggtg atg ttt tat gac ttg gaa ttt gcc gat ata cta 533
Met Phe Tyr Asp Leu Glu Phe Ala Asp Ile Leu
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acg ccg ctc cgc gaa cag ctt cag ttc tgc ctg atg att gaa gcg ggt 581
Thr Pro Leu Arg Glu Gln Leu Gln Phe Cys Leu Met Ile Glu Ala Gly
15 20 25
gcg gga atg aac acg act gaa cag ttt gag agc tta ttt aaa aac agg 629
Ala Gly Met Asn Thr Thr Glu Gln Phe Glu Ser Leu Phe Lys Asn Arg
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ccg ctg aag gtg gaa gct gag cag gtg aca gag cat gat ttg gct tta 677
Pro Leu Lys Val Glu Ala Glu Gln Val Thr Glu His Asp Leu Ala Leu
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atg ctg ttc acc tcg ggc acg acg gga aac ccg aaa ggc tgc atg gtc 725
Met Leu Phe Thr Ser Gly Thr Thr Gly Asn Pro Lys Gly Cys Met Val
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aac cac ggc agt ctg gcc gca tac ttg aca gag gtg aac gtg aaa tcg 773
Asn His Gly Ser Leu Ala Ala Tyr Leu Thr Glu Val Asn Val Lys Ser
80 85 90
aag cag ctg aaa ggc acg cgc ttt tta gcg agc cac ccg ctc tat cat 821
Lys Gln Leu Lys Gly Thr Arg Phe Leu Ala Ser His Pro Leu Tyr His
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atg agc tcg ctc aac cat gtt ttt cag gcg gct ttt gaa gga att gcc 869
Met Ser Ser Leu Asn His Val Phe Gln Ala Ala Phe Glu Gly Ile Ala
110 115 120
ctt tat ttc tta tgg gat ccc gaa ccg ttt gaa atc ctg cag gag atc 917
Leu Tyr Phe Leu Trp Asp Pro Glu Pro Phe Glu Ile Leu Gln Glu Ile
125 130 135
gag aag aaa cgc att cat atg atg atg gcg ttt cct tcc gtc tac acc 965
Glu Lys Lys Arg Ile His Met Met Met Ala Phe Pro Ser Val Tyr Thr
140 145 150 155
tac atg ctg gag gaa atg aaa aga cat cca ttc gac ctg tca tct gtg 1013
Tyr Met Leu Glu Glu Met Lys Arg His Pro Phe Asp Leu Ser Ser Val
160 165 170
aaa atg ctt gtt tcc ggc ggc acc aag gtg ccg gcg cgg ctg att aag 1061
Lys Met Leu Val Ser Gly Gly Thr Lys Val Pro Ala Arg Leu Ile Lys
175 180 185
gag tac aat gac cat gga atc atg atg gtg cag ggg tac ggc agc aca 1109
Glu Tyr Asn Asp His Gly Ile Met Met Val Gln Gly Tyr Gly Ser Thr
190 195 200
gaa gca tgg acg gtc agc gta tgg cgg cct gac atg ggc tgg gat aaa 1157
Glu Ala Trp Thr Val Ser Val Trp Arg Pro Asp Met Gly Trp Asp Lys
205 210 215
gtc act tca gcc ggc aag ccg att ccg caa gtc agc ata aaa atc gaa 1205

10294.000.ST25.txt

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 Asp Pro Asp Thr His Glu Glu Leu Pro Thr Gly Glu Val Gly Glu Val
 240 245 250
 gtc gtc aaa agc ccg tat gtt ttt gaa ggg tat tac caa aat cct tcc 1301
 Val Val Lys Ser Pro Tyr Val Phe Glu Gly Tyr Tyr Gln Asn Pro Ser
 255 260 265
 gcc acg caa aag gtg ctg aaa gac ggc tgg ttc tat atg ggg gac tcc 1349
 Ala Thr Gln Lys Val Leu Lys Asp Gly Trp Phe Tyr Met Gly Asp Ser
 270 275 280
 ggc aaa ctc gat gaa gac gga ttt tta tat att acc ggc cgg tat aaa 1397
 Gly Lys Leu Asp Glu Asp Gly Phe Leu Tyr Ile Thr Gly Arg Tyr Lys
 285 290 295
 gac gtc att gtc tac gga ggc gac aac att tat ccg gac caa gtg gaa 1445
 Asp Val Ile Val Tyr Gly Gly Asp Asn Ile Tyr Pro Asp Gln Val Glu
 300 305 310 315
 gaa atc atc gat caa gtg ccc gga gta gtt gaa tct gcc gtc atc ggc 1493
 Glu Ile Ile Asp Gln Val Pro Gly Val Val Glu Ser Ala Val Ile Gly
 320 325 330
 gtc ccg gat gaa atg tac ggc gag gtt ccg agg gcg tat gtg gtg aaa 1541
 Val Pro Asp Glu Met Tyr Gly Glu Val Pro Arg Ala Tyr Val Val Lys
 335 340 345
 aat gaa agc gcc ggc ctc aag aag gag gac att atc gcg tat tgc aaa 1589
 Asn Glu Ser Ala Gly Leu Lys Lys Glu Asp Ile Ile Ala Tyr Cys Lys
 350 355 360
 gag cgc ctg tcc gac tat aaa att cct gaa atc gtc ttt atc gac agc 1637
 Glu Arg Leu Ser Asp Tyr Lys Ile Pro Glu Ile Val Phe Ile Asp Ser
 365 370 375
 ctt ccg aaa aac agg ctc ggc aaa atc gtc aaa aaa gat ctg cgt gaa 1685
 Leu Pro Lys Asn Arg Leu Gly Lys Ile Val Lys Lys Asp Leu Arg Glu
 380 385 390 395
 ctg gca gtc aaa ggg cag tgagcgcaat gattgaccga aagcttatcc 1733
 Leu Ala Val Lys Gly Gln
 400
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 tcctctcgcc ttacagtatt cagcaggcac ttttgatgac ggcaaacggt gccgcgggag 2093
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<211> 401

<212> PRT

<213> Bacillus licheniformis

<400> 68

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 Thr Glu Gln Phe Glu Ser Leu Phe Lys Asn Arg Pro Leu Lys Val Glu
 35 40 45
 Ala Glu Gln Val Thr Glu His Asp Leu Ala Leu Met Leu Phe Thr Ser
 50 55 60
 Gly Thr Thr Gly Asn Pro Lys Gly Cys Met Val Asn His Gly Ser Leu
 65 70 75 80
 Ala Ala Tyr Leu Thr Glu Val Asn Val Lys Ser Lys Gln Leu Lys Gly
 85 90 95
 Thr Arg Phe Leu Ala Ser His Pro Leu Tyr His Met Ser Ser Leu Asn
 100 105 110
 His Val Phe Gln Ala Ala Phe Glu Gly Ile Ala Leu Tyr Phe Leu Trp
 115 120 125
 Asp Pro Glu Pro Phe Glu Ile Leu Gln Glu Ile Glu Lys Lys Arg Ile
 130 135 140
 His Met Met Met Ala Phe Pro Ser Val Tyr Thr Tyr Met Leu Glu Glu
 145 150 155 160
 Met Lys Arg His Pro Phe Asp Leu Ser Ser Val Lys Met Leu Val Ser
 165 170 175
 Gly Gly Thr Lys Val Pro Ala Arg Leu Ile Lys Glu Tyr Asn Asp His
 180 185 190
 Gly Ile Met Met Val Gln Gly Tyr Gly Ser Thr Glu Ala Trp Thr Val
 195 200 205
 Ser Val Trp Arg Pro Asp Met Gly Trp Asp Lys Val Thr Ser Ala Gly
 210 215 220
 Lys Pro Ile Pro Gln Val Ser Ile Lys Ile Glu Asp Pro Asp Thr His
 225 230 235 240

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Glu Glu Leu Pro Thr Gly Glu Val Gly Glu Val Val Val Lys Ser Pro
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Tyr Val Phe Glu Gly Tyr Tyr Gln Asn Pro Ser Ala Thr Gln Lys Val
260 265 270

Leu Lys Asp Gly Trp Phe Tyr Met Gly Asp Ser Gly Lys Leu Asp Glu
275 280 285

Asp Gly Phe Leu Tyr Ile Thr Gly Arg Tyr Lys Asp Val Ile Val Tyr
290 295 300

Gly Gly Asp Asn Ile Tyr Pro Asp Gln Val Glu Glu Ile Ile Asp Gln
305 310 315 320

Val Pro Gly Val Val Glu Ser Ala Val Ile Gly Val Pro Asp Glu Met
325 330 335

Tyr Gly Glu Val Pro Arg Ala Tyr Val Val Lys Asn Glu Ser Ala Gly
340 345 350

Leu Lys Lys Glu Asp Ile Ile Ala Tyr Cys Lys Glu Arg Leu Ser Asp
355 360 365

Tyr Lys Ile Pro Glu Ile Val Phe Ile Asp Ser Leu Pro Lys Asn Arg
370 375 380

Leu Gly Lys Ile Val Lys Lys Asp Leu Arg Glu Leu Ala Val Lys Gly
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Gln

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<211> 1547

<212> DNA

<213> Bacillus licheniformis

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<221> CDS

<222> (501)..(1046)

<223>

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 tagtgttatg agaaaaaat ccgggaacgg aatcaaggac cataaaaatt ttttctggcc 360
 aacccaaaac cccggtgcgt ttaagtcgtc ataaataaga aaccagcggg ggaataattt 420
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 Leu Lys Lys Leu Ile Val Cys Leu Leu Ala Val
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 tta ctg atc ttg cct gcc gga gcg tcc ctc gca gcg aaa aat caa aca 581
 Leu Leu Ile Leu Pro Ala Gly Ala Ser Leu Ala Ala Lys Asn Gln Thr
 15 20 25
 tca ggg aat tta aca aat aag caa gtc atg caa tta acc ttg cag gca 629
 Ser Gly Asn Leu Thr Asn Lys Gln Val Met Gln Leu Thr Leu Gln Ala
 30 35 40
 cgg gag cac ttt tgg aat acg atg agc ggc cac aat cca aaa gcg aaa 677
 Arg Glu His Phe Trp Asn Thr Met Ser Gly His Asn Pro Lys Ala Lys
 45 50 55
 aac tca act tgc cca tcc aaa aca ttt gaa tac cgc ggt ctt cca tat 725
 Asn Ser Thr Cys Pro Ser Lys Thr Phe Glu Tyr Arg Gly Leu Pro Tyr
 60 65 70 75
 acg tat atg tgc agt gaa ttc agc aca aaa gca aaa tta aca gac tac 773
 Thr Tyr Met Cys Ser Glu Phe Ser Thr Lys Ala Lys Leu Thr Asp Tyr
 80 85 90
 ttg acg ccg gtt ttc aca aaa gac gcc att aaa aaa ggc ttg gaa aaa 821
 Leu Thr Pro Val Phe Thr Lys Asp Ala Ile Lys Lys Gly Leu Glu Lys
 95 100
 tac aac atc att tct tat aaa gga aaa atg gcc gtg cct gtc ggc gat 869
 Tyr Asn Ile Ile Ser Tyr Lys Gly Lys Met Ala Val Pro Val Gly Asp
 110 115 120
 ggg gac aac ctc tta gga tgg gac aag gca aaa atc aaa ctg atc tct 917
 Gly Asp Asn Leu Leu Gly Trp Asp Lys Ala Lys Ile Lys Leu Ile Ser
 125 130 135
 caa aaa aac aat acc cgc act tat gaa ttt tcc gta ccg gca ttg gat 965
 Gln Lys Asn Asn Thr Arg Thr Tyr Glu Phe Ser Val Pro Ala Leu Asp
 140 145 150 155
 gga tcg gtg act gcg aaa aga aag atc acg ttt gtg aaa gaa aac aac 1013
 Gly Ser Val Thr Ala Lys Arg Lys Ile Thr Phe Val Lys Glu Asn Asn
 160 165 170
 aaa tgg aaa atc aat cag ctc gat gct gcc atc taaacgaaaa agctaattgtc 1066
 Lys Trp Lys Ile Asn Gln Leu Asp Ala Ala Ile
 175 180
 taaaaacgga cattagcttt tttccgtcaa acggtcagtt caacgatgtt gccgtcagga 1126
 tccagaatga ctctttcata ataccgtct cccgtgacgc gcggctttcc ggcaacctgg 1186
 tatccttcct tttcaaagcg gctcgtcatc tcgtcaacct cttgccgcga ccctaaggaa 1246
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10294.000.ST25.txt

atcagctcaa gccgtgttcc cgattcaaac tggatgaaat atgattcgaa atgctttttc 1366
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 tcctctaaat tgttcgtcca tatggcgatg tgttcgattt tcataaatct ccctccatt 1486
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<211> 182

<212> PRT

<213> Bacillus licheniformis

<400> 70

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 20 25 30
 Asn Lys Gln Val Met Gln Leu Thr Leu Gln Ala Arg Glu His Phe Trp
 35 40 45
 Asn Thr Met Ser Gly His Asn Pro Lys Ala Lys Asn Ser Thr Cys Pro
 50 55 60
 Ser Lys Thr Phe Glu Tyr Arg Gly Leu Pro Tyr Thr Tyr Met Cys Ser
 65 70 75 80
 Glu Phe Ser Thr Lys Ala Lys Leu Thr Asp Tyr Leu Thr Pro Val Phe
 85 90 95
 Thr Lys Asp Ala Ile Lys Lys Gly Leu Glu Lys Tyr Asn Ile Ile Ser
 100 105 110
 Tyr Lys Gly Lys Met Ala Val Pro Val Gly Asp Gly Asp Asn Leu Leu
 115 120 125
 Gly Trp Asp Lys Ala Lys Ile Lys Leu Ile Ser Gln Lys Asn Asn Thr
 130 135 140
 Arg Thr Tyr Glu Phe Ser Val Pro Ala Leu Asp Gly Ser Val Thr Ala
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 Lys Arg Lys Ile Thr Phe Val Lys Glu Asn Asn Lys Trp Lys Ile Asn
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Gln Leu Asp Ala Ala Ile
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<222> (271)..(1122)
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			Asp	Glu	Lys	Lys	His	Arg	His	Leu						390
			1				5									438
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Ala	Asp	Ser	Cys	Asp	Ala	Arg	Arg	Ser	Phe	Glu	Leu	Pro	Arg	Gly	Ile	
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tggt	gta	tcg	aga	tct	tta	tta	gag	ccg	att	ctc	tat	cat	cac	gcc	ttc	438
Trp	Val	Ser	Arg	Ser	Leu	Leu	Glu	Pro	Ile	Leu	Tyr	His	His	Ala	Phe	
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ccg	tgc	agg	gta	tgg	ccg	gac	atc	gaa	aga	aat	cgg	gga	cag	ttt	gga	486
Pro	Cys	Arg	Val	Trp	Pro	Asp	Ile	Glu	Arg	Asn	Arg	Gly	Gln	Phe	Gly	
			60					65					70			
act	tgc	ctg	cta	tta	cat	atg	aaa	ctg	ctt	gat	cat	tta	aat	atc	aag	534
Thr	Cys	Leu	Leu	Leu	His	Met	Lys	Leu	Leu	Asp	His	Leu	Asn	Ile	Lys	
		75					80					85				
aaa	gtt	cat	gtg	gtt	gcg	gtg	tca	gcc	ggc	ggg	cca	agc	gga	ata	tgt	582
Lys	Val	His	Val	Val	Ala	Val	Ser	Ala	Gly	Gly	Pro	Ser	Gly	Ile	Cys	
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Phe	Ala	Ser	Lys	Tyr	Ser	Glu	Arg	Val	Glu	Ser	Leu	Ile	Leu	Gln	Ser	
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gct	gtc	aca	aag	cag	tgg	ctg	aca	gcg	aag	gat	att	gaa	tat	aaa	gtt	678
Ala	Val	Thr	Lys	Gln	Trp	Leu	Thr	Ala	Lys	Asp	Ile	Glu	Tyr	Lys	Val	
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Gly Gln Ile Ile Phe Arg Pro Pro Val Glu Lys Ala Val Trp Lys Leu
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ata tcg gcg ctt aac aat cga ttt ccg gaa tgg atc ttt aag aaa atg      774
Ile Ser Ala Leu Asn Asn Arg Phe Pro Glu Trp Ile Phe Lys Lys Met
155                               160                               165

cta tcc tcc ttt act aca ctt cct gct gat cag gcg atg ctg aaa gtc      822
Leu Ser Ser Phe Thr Thr Leu Pro Ala Asp Gln Ala Met Leu Lys Val
170                               175                               180

acg gag gga gat att gaa gaa atg aga aaa atg aac aac aga cag cgt      870
Thr Glu Gly Asp Ile Glu Glu Met Arg Lys Met Asn Asn Arg Gln Arg
185                               190                               195

tca agt cga ggg ttc ttg ctt gat tta aaa aat ata gac gat tta tct      918
Ser Ser Arg Gly Phe Leu Leu Asp Leu Lys Asn Ile Asp Asp Leu Ser
205                               210                               215

ttc cat cat ttg aag gag att tct tgt ccg gta tta att atg cat tgc      966
Phe His His Leu Lys Glu Ile Ser Cys Pro Val Leu Ile Met His Cys
220                               225                               230

cga tat gat cgt gtt gtt cca gcc gag cat gct ttt cat gca aaa aaa      1014
Arg Tyr Asp Arg Val Val Pro Ala Glu His Ala Phe His Ala Lys Lys
235                               240                               245

ctg att cct ttt tca gaa gtc tat cag gca gac agc tgg ggt cat ctc      1062
Leu Ile Pro Phe Ser Glu Val Tyr Gln Ala Asp Ser Trp Gly His Leu
250                               255                               260

att tgg ctg gga aca gag ggt aaa tct gtc tca cag aag gtc atc agc      1110
Ile Trp Leu Gly Thr Glu Gly Lys Ser Val Ser Gln Lys Val Ile Ser
265                               270                               275

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Phe Leu Lys Thr

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acagaactga tgaacgtcgt acaagacttg caaataagat gaatgagaaa tcctccctgg      1282

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<210> 72
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<213> Bacillus licheniformis

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<400> 72

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 35 40 45
 Pro Ile Leu Tyr His His Ala Phe Pro Cys Arg Val Trp Pro Asp Ile
 50 55 60
 Glu Arg Asn Arg Gly Gln Phe Gly Thr Cys Leu Leu Leu His Met Lys
 65 70 75 80
 Leu Leu Asp His Leu Asn Ile Lys Lys Val His Val Val Ala Val Ser
 85 90 95
 Ala Gly Gly Pro Ser Gly Ile Cys Phe Ala Ser Lys Tyr Ser Glu Arg
 100 105 110
 Val Glu Ser Leu Ile Leu Gln Ser Ala Val Thr Lys Gln Trp Leu Thr
 115 120 125
 Ala Lys Asp Ile Glu Tyr Lys Val Gly Gln Ile Ile Phe Arg Pro Pro
 130 135 140
 Val Glu Lys Ala Val Trp Lys Leu Ile Ser Ala Leu Asn Asn Arg Phe
 145 150 155 160
 Pro Glu Trp Ile Phe Lys Lys Met Leu Ser Ser Phe Thr Thr Leu Pro
 165 170 175
 Ala Asp Gln Ala Met Leu Lys Val Thr Glu Gly Asp Ile Glu Glu Met
 180 185 190
 Arg Lys Met Asn Asn Arg Gln Arg Ser Ser Arg Gly Phe Leu Leu Asp
 195 200 205
 Leu Lys Asn Ile Asp Asp Leu Ser Phe His His Leu Lys Glu Ile Ser
 210 215 220
 Cys Pro Val Leu Ile Met His Cys Arg Tyr Asp Arg Val Val Pro Ala
 225 230 235 240
 Glu His Ala Phe His Ala Lys Lys Leu Ile Pro Phe Ser Glu Val Tyr
 245 250 255
 Gln Ala Asp Ser Trp Gly His Leu Ile Trp Leu Gly Thr Glu Gly Lys
 260 265 270

Ser Val Ser Gln Lys Val Ile Ser Phe Leu Lys Thr
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<210> 73

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<213> Bacillus licheniformis

<220>

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<222> (256)..(1131)

<223>

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 tttttggcca ttatatgaat tcggccagcg ttgaatatTT cctcttttca gggaaatttc 180
 cgaagcggcg attcaaaaat ccgcaaactt atcttacaat agaaaaagtt ctgaatgac 240
 gagtagggag agatc gtt agt atg aaa gta tcg gtt ctg ttt gtc ttg ctt 291
 Val Ser Met Lys Val Ser Val Leu Phe Val Leu Leu
 1 5 10
 gcg gca att tta tgg gga acg acg gga aca acc cag gca ttt gcg ccg 339
 Ala Ala Ile Leu Trp Gly Thr Thr Gly Thr Thr Gln Ala Phe Ala Pro
 15 20 25
 aaa gag gcg gca cct ctt gtg ttc ggc gct gtc aga atg gct gtc ggc 387
 Lys Glu Ala Ala Pro Leu Val Phe Gly Ala Val Arg Met Ala Val Gly
 30 35 40
 ggc atc acc ctg ctc ttg ttc gcg gct ttc cgc ggt caa ttg aaa cga 435
 Gly Ile Thr Leu Leu Leu Phe Ala Ala Phe Arg Gly Gln Leu Lys Arg
 45 50 55 60
 agc ggc tgg ccc gtt aaa acg ctg atc atc gca gca ttg agc atg gca 483
 Ser Gly Trp Pro Val Lys Thr Leu Ile Ile Ala Ala Leu Ser Met Ala
 65 70 75
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 Phe Tyr Gln Pro Phe Phe Phe Ser Ala Val Ser Leu Ser Gly Ile Ala
 80 85 90
 gtc gga acg gtc gtc gcc atc ggc agc gct ccg att att gcc ggc tgc 579
 Val Gly Thr Val Val Ala Ile Gly Ser Ala Pro Ile Ile Ala Gly Cys
 95 100 105
 ctc gaa tgg ctg gtg ttc aaa aag gtt ccg cag acg aaa tgg tgg atc 627
 Leu Glu Trp Leu Val Phe Lys Lys Val Pro Gln Thr Lys Trp Trp Ile
 110 115 120
 gca act gct gca gcg ata gca ggc gta gcc tta tta ttc att ccc tcc 675
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Ala Thr Ala Ala Ala Ile Ala Gly Val Ala Leu Leu Phe Ile Pro Ser
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gcc tca tcg ggg ggg agc ttt ctc ggc ata ctg ctc gca ctt ggc gcc 723
Ala Ser Ser Gly Gly Ser Phe Leu Gly Ile Leu Leu Ala Leu Gly Ala 155

ggt ctt tcc ttt gcc gtc tac acg ctg aca agc aag aaa ctc ctg caa 771
Gly Leu Ser Phe Ala Val Tyr Thr Leu Thr Ser Lys Lys Leu Leu Gln 160 170

aag caa aag ccg gag gct gtc aca ggc acc gta ttc ttt tta agc gct 819
Lys Gln Lys Pro Glu Ala Val Thr Gly Thr Val Phe Phe Leu Ser Ala 175 185

gta ttg ctt gcc ccg ttg ttg ttt ctg tac gat ctc ggc tgg atc tca 867
Val Leu Leu Ala Pro Leu Leu Phe Leu Tyr Asp Leu Gly Trp Ile Ser 190 200

tcg gtt cag gga atg gct gtc agc ctc tat atc ggg gtc att gca acc 915
Ser Val Gln Gly Met Ala Val Ser Leu Tyr Ile Gly Val Ile Ala Thr 205 210 215 220

gga gcc gcg tac ctg tta ttt acg aca gga ttg gca aaa gtg ccc gcc 963
Gly Ala Ala Tyr Leu Leu Phe Thr Thr Gly Leu Ala Lys Val Pro Ala 225 230 235

tca acg gcg gtg acg ctg tcg ctt gct gaa ccg ctt aca gcg tcg ctg 1011
Ser Thr Ala Val Thr Leu Ser Leu Ala Glu Pro Leu Thr Ala Ser Leu 240 245 250

ttg gga acc gtg ctt gtc agg gaa tcg ctg cct ctt gtt tcc tgg gcc 1059
Leu Gly Thr Val Leu Val Arg Glu Ser Leu Pro Leu Val Ser Trp Ala 255 260 265

ggg atc gcc ctg ctt ctt tta ggc att ttt tat att tcc tat cag ccc 1107
Gly Ile Ala Leu Leu Leu Leu Gly Ile Phe Tyr Ile Ser Tyr Gln Pro 270 275 280

aaa aag gat aaa ata aac gct gaa cagatgaaag cgtaaaaaaa acccgcccgg 1161
Lys Lys Asp Lys Ile Asn Ala Glu 285 290

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ttgtttccaa atacggctcg atgccttcca gtccgctttc gcgtccgata ccgctttcct 1281

tcatgccgcc gaaaggcgcc tgaacgggtg acgggtccgcc gtcattccag ccgagaatgc 1341

cgtaatcaag gtttttcggat aaatagatgc cgcgggcgta gttttccgta aagaagtatg 1401

ccgctaaacc gtaaggcgta tcattggcga gcttgaccgc ttcgtccagc gttttaaaag 1461

acgtaatcgg cgcaacgggg ccgaatgttt cctcatgcat gatcgtcatt gaaggatcaa 1521

catccgtcag cactgtcgga tggacaaagt agcatgattt ctcatcatcg ctttcatatt 1581

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<210> 74

<211> 292

<212> PRT

<213> Bacillus licheniformis

<400> 74

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 20 25 30
 Pro Leu Val Phe Gly Ala Val Arg Met Ala Val Gly Gly Ile Thr Leu
 35 40 45
 Leu Leu Phe Ala Ala Phe Arg Gly Gln Leu Lys Arg Ser Gly Trp Pro
 50 55 60
 Val Lys Thr Leu Ile Ile Ala Ala Leu Ser Met Ala Phe Tyr Gln Pro
 65 70 75 80
 Phe Phe Phe Ser Ala Val Ser Leu Ser Gly Ile Ala Val Gly Thr Val
 85 90 95
 Val Ala Ile Gly Ser Ala Pro Ile Ile Ala Gly Cys Leu Glu Trp Leu
 100 105 110
 Val Phe Lys Lys Val Pro Gln Thr Lys Trp Trp Ile Ala Thr Ala Ala
 115 120 125
 Ala Ile Ala Gly Val Ala Leu Leu Phe Ile Pro Ser Ala Ser Ser Gly
 130 135 140
 Gly Ser Phe Leu Gly Ile Leu Leu Ala Leu Gly Ala Gly Leu Ser Phe
 145 150 155 160
 Ala Val Tyr Thr Leu Thr Ser Lys Lys Leu Leu Gln Lys Gln Lys Pro
 165 170 175
 Glu Ala Val Thr Gly Thr Val Phe Phe Leu Ser Ala Val Leu Leu Ala
 180 185 190
 Pro Leu Leu Phe Leu Tyr Asp Leu Gly Trp Ile Ser Ser Val Gln Gly
 195 200 205
 Met Ala Val Ser Leu Tyr Ile Gly Val Ile Ala Thr Gly Ala Ala Tyr
 210 215 220
 Leu Leu Phe Thr Thr Gly Leu Ala Lys Val Pro Ala Ser Thr Ala Val
 225 230 235 240
 Thr Leu Ser Leu Ala Glu Pro Leu Thr Ala Ser Leu Leu Gly Thr Val
 245 250 255

Leu Val Arg Glu Ser Leu Pro Leu Val Ser Trp Ala Gly Ile Ala Leu
260 265 270

Leu Leu Leu Gly Ile Phe Tyr Ile Ser Tyr Gln Pro Lys Lys Asp Lys
275 280 285

Ile Asn Ala Glu
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<210> 75

<211> 2140

<212> DNA

<213> *Bacillus licheniformis*

<220>

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<222> (501)..(1637)

<223>

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15 20 25

ggt cag gaa gcc atc tat aaa aaa ggc ttg ccc aaa gaa gac agt cca 629
Val Gln Glu Ala Ile Tyr Lys Lys Gly Leu Pro Lys Glu Asp Ser Pro

gca ttt aga gaa ttt atg aga cat gaa ctt gat tta gcg aca gac gca 677
Ala Phe Arg Glu Phe Met Arg His Glu Leu Asp Leu Ala Thr Asp Ala
45 50 55

act ctt agt tat caa aat agt aca tat acg att atg cgc agt gat aaa 725
Thr Leu Ser Tyr Gln Asn Ser Thr Tyr Thr Ile Met Arg Ser Asp Lys
60 65 70 75

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aag ggg cta cgg tac tat caa tat aca gat caa gaa gta gac gat ttt Lys Gly Leu Arg Tyr Tyr Gln Tyr Thr Asp Gln Glu Val Asp Asp Phe 80 85 90	773
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gat ttg aaa aca act gaa ttt tta act aaa gaa aaa ctt atc cac aat Asp Leu Lys Thr Thr Glu Phe Leu Thr Lys Glu Lys Leu Ile His Asn 110 115 120	869
aaa ctt gaa tat aat ctg ccg gaa atg aca tta gat aaa aag aat gtt Lys Leu Glu Tyr Asn Leu Pro Glu Met Thr Leu Asp Lys Lys Asn Val 125 130 135	917
cta aaa gtg aaa aca aaa agc gga gaa aaa aaa ata gag ttt cca tca Leu Lys Val Lys Thr Lys Ser Gly Glu Lys Lys Ile Glu Phe Pro Ser 140 145 150 155	965
gcc aag gat aaa aaa gta cat ctg gcg tta gca gct gtt agc aaa gac Ala Lys Asp Lys Lys Val His Leu Ala Leu Ala Val Ser Lys Asp 160 165 170	1013
agc atg ctt ata caa gtg gac gta tat gaa aaa ttt aaa aat ggt gac Ser Met Leu Ile Gln Val Asp Val Tyr Glu Lys Phe Lys Asn Gly Asp 175 180 185	1061
ctt gga gac aga caa ata tat tat ctt ttt tta aaa agt gat ctt tca Leu Gly Asp Arg Gln Ile Tyr Tyr Leu Phe Leu Lys Ser Asp Leu Ser 190 195 200	1109
aaa tac cgg att gtt aaa gaa gag gaa tta aat tca aca att gag tct Lys Tyr Arg Ile Val Lys Glu Glu Leu Asn Ser Thr Ile Glu Ser 205 210 215	1157
ggg aaa ctg aag gaa tac tta tcc gta ttt cca aat gta gcg aag gat Gly Lys Leu Lys Glu Tyr Leu Ser Val Phe Pro Asn Val Ala Lys Asp 220 225 230 235	1205
gga gca tat cgt aag tta ttt gat aaa tac att ttt gat gaa aag aaa Gly Ala Tyr Arg Lys Leu Phe Asp Lys Tyr Ile Phe Asp Glu Lys Lys 240 245 250	1253
aac aaa gtt agg aaa atc aaa aac act gat att ctg agc aaa gac ggt Asn Lys Val Arg Lys Ile Lys Asn Thr Asp Ile Leu Ser Lys Asp Gly 255 260 265	1301
aag tat gtt tat att aac gga gca aaa gaa aaa gaa aca aat gta atg Lys Tyr Val Tyr Ile Asn Gly Ala Lys Glu Lys Glu Thr Asn Val Met 270 275 280	1349
cct gat ggt atc caa cag ata caa aca atg gat aat tat cta aaa gga Pro Asp Gly Ile Gln Gln Ile Gln Thr Met Asp Asn Tyr Leu Lys Gly 285 290 295	1397
aat gaa aaa tat gaa gct caa ttt aag att gat ttc aaa caa att gca Asn Glu Lys Tyr Glu Ala Gln Phe Lys Ile Asp Phe Lys Gln Ile Ala 300 305 310 315	1445
aaa gag atg gat tta aac gcg ggt gat gcg agg ata gct aat att cat Lys Glu Met Asp Leu Asn Ala Gly Asp Ala Arg Ile Ala Asn Ile His 320 325 330	1493
tat ttt aat aaa gat tat gta gtt ttg tat att tct tat cat ggg aag Tyr Phe Asn Lys Asp Tyr Val Val Leu Tyr Ile Ser Tyr His Gly Lys 335 340 345	1541

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 Thr Ile Gly Thr Ala Gly Ser Val Asn Val Leu Ile Asp Leu Gln Lys
 350 355 360

aac aaa caa cag cca acg gct tat tta gtt gat tta gga att gaa tca 1637
 Asn Lys Gln Gln Pro Thr Ala Tyr Leu Val Asp Leu Gly Ile Glu Ser
 365 370 375

tagagggact gaagagtttt tatgcagtcc ttttcttatt tgacaaaggt aggccacaaa 1697

attgggacaa gccttctgct tcctacttcc ttatccaatt taagagaagt tcttgcagaa 1757

agcgataaat gacgaaagaa tgcagcagcg tttggaacac tcgttaatgc tcgtttcggg 1817

agcggacgga aaaatcgtcg gctttgccaa ctactccttt gtcagagaag gaggggtagc 1877

ctatctcgca gccgtttatt tagctccgga ataccagggg aaaggcatcg gaaccgcatt 1937

attggaagag gggatgaacc atttaaaggg agtgaaaaag atctttgtag aggttgaaaa 1997

agaaaaccgc accggaaaaa acttttacaa ggcgaagggg tttgaggatg tcgccgaata 2057

tgatgaagat ttcgaagggc atatcctcaa aacagtcaga atggccttgc acgtataatc 2117

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<210> 76

<211> 379

<212> PRT

<213> Bacillus licheniformis

<400> 76

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Tyr Lys Lys Gly Leu Pro Lys Glu Asp Ser Pro Ala Phe Arg Glu Phe
 35 40 45

Met Arg His Glu Leu Asp Leu Ala Thr Asp Ala Thr Leu Ser Tyr Gln
 50 55 60

Asn Ser Thr Tyr Thr Ile Met Arg Ser Asp Lys Lys Gly Leu Arg Tyr
 65 70 75 80

Tyr Gln Tyr Thr Asp Gln Glu Val Asp Asp Phe Tyr Ser Pro Phe Leu
 85 90 95

Ser Ala Asn Lys Tyr Pro Ala Thr Lys Leu Tyr Asp Leu Lys Thr Thr
 100 105 110

Glu Phe Leu Thr Lys Glu Lys Leu Ile His Asn Lys Leu Glu Tyr Asn
 115 120 125

Leu Pro Glu Met Thr Leu Asp Lys Lys Asn Val Leu Lys Val Lys Thr
 130 135 140

Lys Ser Gly Glu Lys Lys Ile Glu Phe Pro Ser Ala Lys Asp Lys Lys
 145 150 160

Val His Leu Ala Leu Ala Ala Val Ser Lys Asp Ser Met Leu Ile Gln
 165 170 175

Val Asp Val Tyr Glu Lys Phe Lys Asn Gly Asp Leu Gly Asp Arg Gln
 180 185 190

Ile Tyr Tyr Leu Phe Leu Lys Ser Asp Leu Ser Lys Tyr Arg Ile Val
 195 200 205

Lys Glu Glu Glu Leu Asn Ser Thr Ile Glu Ser Gly Lys Leu Lys Glu
 210 215 220

Tyr Leu Ser Val Phe Pro Asn Val Ala Lys Asp Gly Ala Tyr Arg Lys
 225 230 235 240

Leu Phe Asp Lys Tyr Ile Phe Asp Glu Lys Lys Asn Lys Val Arg Lys
 245 250 255

Ile Lys Asn Thr Asp Ile Leu Ser Lys Asp Gly Lys Tyr Val Tyr Ile
 260 265 270

Asn Gly Ala Lys Glu Lys Glu Thr Asn Val Met Pro Asp Gly Ile Gln
 275 280 285

Gln Ile Gln Thr Met Asp Asn Tyr Leu Lys Gly Asn Glu Lys Tyr Glu
 290 295 300

Ala Gln Phe Lys Ile Asp Phe Lys Gln Ile Ala Lys Glu Met Asp Leu
 305 310 315 320

Asn Ala Gly Asp Ala Arg Ile Ala Asn Ile His Tyr Phe Asn Lys Asp
 325 330 335

Tyr Val Val Leu Tyr Ile Ser Tyr His Gly Lys Thr Ile Gly Thr Ala
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<210> 77

<211> 1387

<212> DNA

<213> *Bacillus licheniformis*

<220>

<221> CDS

<222> (501)..(884)

<223>

<400> 77

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acgcaaattgt agttgatgag ttaaacgtat ttccggttcc ggacggagat acgggaacga      240
acactaatct gtcgatgaca tccggtgcga aagaagtggg gcaaactgac accgccaata      300
tcggcaaagt ggcacaaagc ctgtcaaggg ggcttctgat gggggcgagg ggaaactcgg      360
gcgtcatttt atcccagctg ttcagaggct ttggcaaatac gattgaacag aaatcggaaa      420
ttaacgcgaa agaatttgcc gccgcgttcc aggccggagt ggacaccgcc tacaaggccg      480
tcataaaciaa gcttctacag atg tct acc agc agc att gtc gtt ctc ttg att      533
                    Met Ser Thr Ser Ser Ile Val Val Leu Leu Ile
                    1           5           10

tgc gcc gcg ctc atc atc tac gcg gtc gct tca tac atc tat cag cag      581
cys ala ala leu ile ile tyr ala val ala ser tyr ile tyr gln gln
                    15           20           25

cgc att atg aaa acc ttg aca gaa gaa gaa ttc cgg gca ggc tat cgc      629
arg ile met lys thr leu thr glu glu glu phe arg ala gly tyr arg
                    30           35           40

aaa gcg cag ctc atc gat gtg cgc gag ccg aat gag tat gaa ggc ggc      677
lys ala gln leu ile asp val arg glu pro asn glu tyr glu gly gly
                    45           50           55

cac att ttg ggt gcg aga aac att ccg ctt tca cag ctt aag caa aga      725
his ile leu gly ala arg asn ile pro leu ser gln leu lys gln arg
                    60           65           70           75

aaa agc gaa atc cgg cct gac aaa ccg gtt tac ctg tac tgc caa aac      773
lys ser glu ile arg pro asp lys pro val tyr leu tyr cys gln asn
                    80           85           90

aac gtc aga agc gga agg gcc gcc caa acg ctc cgc aaa cac ggc tgt      821
asn val arg ser gly arg ala ala gln thr leu arg lys his gly cys
                    95           100           105

aag gag att tac aac ctg aaa ggc ggg ttc aaa aaa tgg ggc gga aaa      869
lys glu ile tyr asn leu lys gly gly phe lys lys trp gly gly lys
                    110           115           120

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10294.000.ST25.txt

att aaa acg aaa aat taataaccga agctgtctct gctatggaag gcttcagttg 924
 ile Lys Thr Lys Asn
 125

agtccagcat cctaaagcgg ttttaacgttt taggatgttt tttttgcatc cgggaggatt 984
 cgggtgatga gcggttatcc ctttccggca aaaataagcc ggcgagatgg gttcgccggc 1044
 tttgttcgtt attttttcaa gtcttcgatt gaattgacat ctttcatata tgtcggaaacg 1104
 acaaggccaa tttttacgcc tgtcatgcta gtaccgatat cttcgtattt gcctttgtat 1164
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 ccattttgca tgccagggtca catcgggcct gcttctactt gggctgagcg tacgggtgtat 1284
 ccctagtctt caagaacttt gcgatgacat tcgtgctcgc attttcgctg tcccatgccca 1344
 catagccgag ctttaattttt tcaccgtccg cttatcgacg ccc 1387

<210> 78

<211> 128

<212> PRT

<213> Bacillus licheniformis

<400> 78

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Ile Tyr Ala Val Ala Ser Tyr ile Tyr Gln Gln Arg ile Met Lys Thr
 20 25 30

Leu Thr Glu Glu Glu Phe Arg Ala Gly Tyr Arg Lys Ala Gln Leu ile
 35 40 45

Asp Val Arg Glu Pro Asn Glu Tyr Glu Gly Gly His ile Leu Gly Ala
 50 55 60

Arg Asn ile Pro Leu Ser Gln Leu Lys Gln Arg Lys Ser Glu ile Arg
 65 70 75 80

Pro Asp Lys Pro Val Tyr Leu Tyr Cys Gln Asn Asn Val Arg Ser Gly
 85 90 95

Arg Ala Ala Gln Thr Leu Arg Lys His Gly Cys Lys Glu ile Tyr Asn
 100 105 110

Leu Lys Gly Gly Phe Lys Lys Trp Gly Gly Lys ile Lys Thr Lys Asn
 115 120 125

<210> 79

<211> 1486

<212> DNA

<213> *Bacillus licheniformis*

<220>

<221> CDS

<222> (501)..(983)

<223>

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gat ggg cag tac agt tta agc tat gtg gac ttt ata aac gga aaa att 965
Asp Gly Gln Tyr Ser Leu Ser Tyr Val Asp Phe Ile Asn Gly Lys Ile
140 145 150 155

cac aaa aat att acg cct tagacgaaac aggggggaaat cgagttgaat 1013
His Lys Asn Ile Thr Pro
160

ctagctaaaa gagtatcagc gttaacacca tctgcaacat tggcaatcac tgcaaaagca 1073
aaagaattaa aagcggcagg gcacgacgtc atcgggtcttg gggcagggtga gccggatttt 1133
aatacgcttg agcacatcat tgaagcggct gtccgttcga tgaacgaagg acataccaaa 1193
tacacgcctt ccggcgggtct tgcggcgctg aaagacagca tccgcgataa attcaagcgc 1253
gatcagggaa ttgaatacag ccaatcgga gttattgtgt gcacagggtgc aaagcatgct 1313
ctttacaccc tatttcaagt gtcctcgcac gaaggggacg aagtgattat tccgactccg 1373
tactgggtca gctatcctga acaagtcaag cttgcaggcg gcaaacctgt gtttgtggaa 1433
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<210> 80
<211> 161
<212> PRT
<213> Bacillus licheniformis

<400> 80
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Gln Lys Glu Asn Gly His Glu Gln Ala Ala Glu Thr Ala Arg Gln Glu
35 40 45
Ala Gly Leu Lys Gln Val Asp Ser Val Glu Thr Phe Val Gly Lys Glu
50 55 60
Lys Gln Tyr Ile Val Thr Gly Ala Asp Lys Lys Gly Asp Lys Met Tyr
65 70 75 80
Val Trp Val Pro Ala Asp Lys Lys Gln Lys Thr Leu Tyr Lys Lys Ala
85 90 95
Ser Ala Gly Ile Thr Gly Arg Gln Ala Ala Lys Ala Val Gln Asp Glu
100 105 110

Gly Leu Met Ser Glu Leu Lys Glu Val His Leu Ala Arg Glu Gly Asn
 115 120 125

Val Leu Leu Trp Glu Val Thr Tyr Leu Asn Lys Asp Gly Gln Tyr Ser
 130 135 140

Leu Ser Tyr Val Asp Phe Ile Asn Gly Lys Ile His Lys Asn Ile Thr
 145 150 155 160

Pro

<210> 81

<211> 1993

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1490)

<223>

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 ctcttttttag cttcgggaag ctttaaggtc atggccgtct ccattttgat tgcaactgct 180
 gtttcgatag cggcatccat tctattgaca aggggtgttg gtaagcgtat gaaatttttt 240
 aaaaaattga tcttaaccga ctcgacaagc acagaaagcg gatacgtgtc aaatgaaagc 300
 cggcgcgatt taattggcaa aatcggcgtc acgtatacac cgctcagacc gtccggaacg 360
 gtcacatcgc acgatgaacg gcttgatggt gtatctgaag gctcgttcac cgcaaaggat 420
 aagaaagtga aagtgggttaa agtgggaaggc tcacgcattg ttgtgagaga attataaatt 480
 acatttttag gaggaatata atg gat ccg tca aca ctg ttt ctt tta ctt att 533
 Met Asp Pro Ser Thr Leu Phe Leu Leu Ile
 1 5 10
 atc gca gcc gga atc atc cta cta gct gtc ttc ttt aca ttc gtc ccg 581
 Ile Ala Ala Gly Ile Ile Leu Leu Ala Val Phe Phe Thr Phe Val Pro
 15 20 25
 gtc atg ctg tgg atc tcg gct ttg gcc gct ggt gtt aaa atc agc att 629
 Val Met Leu Trp Ile Ser Ala Leu Ala Ala Gly Val Lys Ile Ser Ile
 30 35 40
 ttc aca ctg atc gga atg agg ctc cgc cgc gtc att cca aac cgc gtg 677
 Phe Thr Leu Ile Gly Met Arg Leu Arg Arg Val Ile Pro Asn Arg Val
 45 50 55

10294.000.ST25.txt

gtg Val 60	aac Asn	ccg Pro	ctc Leu	atc Ile	aaa Lys 65	gcg Ala	cac His	aaa Lys	gcg Ala	gga Gly 70	ctt Leu	gat Asp	gtt Val	gcc Ala 75	atc Ile	725
aat Asn	cag Gln	ctg Leu	gaa Glu	agc Ser 80	cac His	tat Tyr	ctt Leu	gca Ala	ggg Gly 85	ggt Gly	aat Asn	gtt Val	gac Asp	cgg Arg 90	gtc Val	773
gtc Val	aac Asn	gcg Ala	ctt Leu 95	atc Ile	gct Ala	gcc Ala	caa Gln	cgt Arg 100	gca Ala	aac Asn	att Ile	gaa Glu 105	ctt Leu	aca Thr	ttc Phe	821
gcc Ala	aga Arg	tgt Cys 110	gcg Ala	gcc Ala	atc Ile	gat Asp	tta Leu 115	gcg Ala	ggc Gly	cgt Arg	gac Asp	gtg Val 120	ctt Leu	gaa Glu	gcc Ala	869
gtt Val	caa Gln 125	atg Met	agc Ser	gtt Val	aat Asn	ccg Pro 130	aaa Lys	gtc Val	atc Ile	gaa Glu 135	acg Thr	ccg Pro	ttt Phe	att Ile	gcc Ala	917
ggt Gly 140	gta Val	gca Ala	atg Met	gat Asp	ggt Gly 145	atc Ile	gaa Glu	gtg Val	aaa Lys	gca Ala 150	aaa Lys	gcg Ala	aga Arg	atc Ile	acg Thr 155	965
gtt Val	cgc Arg	gct Ala	aac Asn	atc Ile 160	gac Asp	cgc Arg	ctt Leu	gtc Val	ggg Gly 165	gga Gly	gcg Ala	ggc Gly	gaa Glu	gaa Glu 170	acg Thr	1013
atc Ile	att Ile	gcc Ala	cgt Arg 175	gtc Val	ggc Gly	gaa Glu	ggg Gly	atc Ile 180	gtt Val	tcg Ser	aca Thr	atc Ile	ggt Gly 185	tct Ser	tcc Ser	1061
gat Asp	aat Asn	cat His 190	aaa Lys	aaa Lys	gtg Val	ctt Leu	gaa Glu 195	aac Asn	cca Pro	gat Asp	atg Met	att Ile 200	tca Ser	caa Gln	acc Thr	1109
gta Val	ttg Leu 205	agc Ser	aaa Lys	ggg Gly	ttg Leu	gat Asp 210	tca Ser	ggt Gly	aca Thr	gcg Ala	ttt Phe 215	gaa Glu	att Ile	cta Leu	tcg Ser	1157
atc Ile 220	gat Asp	atc Ile	gct Ala	gac Asp	gtt Val 225	gac Asp	atc Ile	ggc Gly	aaa Lys	aac Asn 230	atc Ile	gga Gly	gcg Ala	att Ile	ctg Leu 235	1205
caa Gln	acc Thr	gac Asp	cag Gln	gct Ala 240	gaa Glu	gcc Ala	gat Asp	aaa Lys	aac Asn 245	atc Ile	gcc Ala	cag Gln	gcg Ala	aaa Lys 250	gcg Ala	1253
gaa Glu	gag Glu	cgc Arg	cgc Arg 255	gcc Ala	atg Met	gcg Ala	gtt Val	gcg Ala 260	caa Gln	gaa Glu	cag Gln	gaa Glu	atg Met 265	cgc Arg	gcc Ala	1301
cgc Arg	gtc Val	gaa Glu 270	gaa Glu	atg Met	cgc Arg	gcc Ala	aaa Lys 275	gtc Val	gtc Val	gaa Glu	gcc Ala	gaa Glu	gcc Ala	gaa Glu	gtg Val	1349
ccg Pro	ctt Leu 285	gca Ala	atg Met	tct Ser	gaa Glu	gct Ala 290	ctc Leu	cgc Arg	agc Ser	gga Gly	aaa Lys 295	atc Ile	ggc Gly	gtc Val	atg Met	1397
gac Asp 300	tac Tyr	ctc Leu	aat Asn	atg Met	aaa Lys 305	aac Asn	atc Ile	gac Asp	gcc Ala	gac Asp 310	act Thr	gac Asp	atg Met	cgc Arg	gat Asp 315	1445
tct Ser	ttc Phe	gga Gly	aag Lys	atg Met 320	acg Thr	aaa Lys	gac Asp	caa Gln	aat Asn 325	gaa Glu	gag Glu	gat Asp	cat His	aaa Lys 330		1490

10294.000.ST25.txt

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 agccgaaaca gacggcgag caccgtcctg caaaaaataa aaaccagcgg ccggcagcgg 1730
 cagctgcaaa cagcgcagat atggaagcag agctccgcag aatcaaagaa gatgccgagc 1790
 gttccatgcc ggccgttgaa cggaccatta aaaagcagag cagccgggtg atcaaccgga 1850
 agcaagagct gctcgacatg aataaaaaaa caatagttca aggcattgtc ctcaagtgaag 1910
 tattcggccc tccgcggtcg agaaagccgc attacacaat gaggcgccgg cctaaaattt 1970
 aagtattaga acccccttct cac 1993

<210> 82

<211> 330

<212> PRT

<213> Bacillus licheniformis

<400> 82

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 Ser Ala Leu Ala Ala Gly Val Lys Ile Ser Ile Phe Thr Leu Ile Gly
 35 40 45
 Met Arg Leu Arg Arg Val Ile Pro Asn Arg Val Val Asn Pro Leu Ile
 50 55 60
 Lys Ala His Lys Ala Gly Leu Asp Val Ala Ile Asn Gln Leu Glu Ser
 65 70 75 80
 His Tyr Leu Ala Gly Gly Asn Val Asp Arg Val Val Asn Ala Leu Ile
 85 90 95
 Ala Ala Gln Arg Ala Asn Ile Glu Leu Thr Phe Ala Arg Cys Ala Ala
 100 105 110
 Ile Asp Leu Ala Gly Arg Asp Val Leu Glu Ala Val Gln Met Ser Val
 115 120 125
 Asn Pro Lys Val Ile Glu Thr Pro Phe Ile Ala Gly Val Ala Met Asp
 130 135 140

Gly Ile Glu Val Lys Ala Lys Ala Arg Ile Thr Val Arg Ala Asn Ile
 145 150 155 160

Asp Arg Leu Val Gly Gly Ala Gly Glu Glu Thr Ile Ile Ala Arg Val
 165 170 175

Gly Glu Gly Ile Val Ser Thr Ile Gly Ser Ser Asp Asn His Lys Lys
 180 185 190

Val Leu Glu Asn Pro Asp Met Ile Ser Gln Thr Val Leu Ser Lys Gly
 195 200 205

Leu Asp Ser Gly Thr Ala Phe Glu Ile Leu Ser Ile Asp Ile Ala Asp
 210 215 220

Val Asp Ile Gly Lys Asn Ile Gly Ala Ile Leu Gln Thr Asp Gln Ala
 225 230 235 240

Glu Ala Asp Lys Asn Ile Ala Gln Ala Lys Ala Glu Glu Arg Arg Ala
 245 250 255

Met Ala Val Ala Gln Glu Gln Glu Met Arg Ala Arg Val Glu Glu Met
 260 265 270

Arg Ala Lys Val Val Glu Ala Glu Ala Glu Val Pro Leu Ala Met Ser
 275 280 285

Glu Ala Leu Arg Ser Gly Lys Ile Gly Val Met Asp Tyr Leu Asn Met
 290 295 300

Lys Asn Ile Asp Ala Asp Thr Asp Met Arg Asp Ser Phe Gly Lys Met
 305 310 315 320

Thr Lys Asp Gln Asn Glu Glu Asp His Lys
 325 330

<210> 83

<211> 1705

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (308)..(1237)

<223>

10294.000.ST25.txt

<400> 83
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 gtgacggccc tcattgcaat ggagaagtca gttgccgttc ttatcggttc gattgtttgg 240
 ttcacggcgg tttcgcagct ctttttttct cttctattga aacagatcag gccataccaa 300
 aaaggag gaa tac aaa atg agt caa gtc gaa ttt gaa ggt gta agt aaa 349
 Glu Tyr Lys Met Ser Gln Val Glu Phe Glu Gly Val Ser Lys
 1 5 10
 cga ata aaa ggc aga cca att gtc caa aat atc aca ttt caa att gcc 397
 Arg Ile Lys Gly Arg Pro Ile Val Gln Asn Ile Thr Phe Gln Ile Ala
 15 20 25 30
 cca ggt aca att ttt ggg ctg ctc ggg cca aac ggc gct ggc aag aca 445
 Pro Gly Thr Ile Phe Gly Leu Leu Gly Pro Asn Gly Ala Gly Lys Thr
 35 40 45
 aca ctt atc aaa atg att gtc ggg atg gca aag ccg aca tca gga gat 493
 Thr Leu Ile Lys Met Ile Val Gly Met Ala Lys Pro Thr Ser Gly Asp
 50 55 60
 atc cgc atc gac ggc tat tca gtt aaa agc aat tac gag gaa gcg gca 541
 Ile Arg Ile Asp Gly Tyr Ser Val Lys Ser Asn Tyr Glu Glu Ala Ala
 65 70 75
 gcc cga gtc ggt tct gtt gtt gaa aac cca tcc ttt tat gag cac tta 589
 Ala Arg Val Gly Ser Val Val Glu Asn Pro Ser Phe Tyr Glu His Leu
 80 85 90
 aca gga tac caa aac ctt aaa tat ctc ggc gga ttc cac agc cac gtg 637
 Thr Gly Tyr Gln Asn Leu Lys Tyr Leu Gly Gly Phe His Ser His Val
 95 100 105 110
 tca aag gag cgc ata gaa gag atc gtt cag ctt gtt gat ttg aca gga 685
 Ser Lys Glu Arg Ile Glu Glu Ile Val Gln Leu Val Asp Leu Thr Gly
 115 120 125
 agt att cat aaa cca gtt aaa acg tat tca tta ggc atg aaa cag cgt 733
 Ser Ile His Lys Pro Val Lys Thr Tyr Ser Leu Gly Met Lys Gln Arg
 130 135 140
 ttg ggc ctt gcc gtc gcg ctc ttg cat gat ccg gaa ttt ctc att ctc 781
 Leu Gly Leu Ala Val Ala Leu Leu His Asp Pro Glu Phe Leu Ile Leu
 145 150 155
 gat gaa ccg aca aac ggc ctt gat cct cag gga atc att gat ttg cgc 829
 Asp Glu Pro Thr Asn Gly Leu Asp Pro Gln Gly Ile Ile Asp Leu Arg
 160 165 170
 gaa cac ctt cag tac ttg gcg aaa acc ttc aac aaa acg att ttg att 877
 Glu His Leu Gln Tyr Leu Ala Lys Thr Phe Asn Lys Thr Ile Leu Ile
 175 180 185 190
 tcg agt cat ctt ctg tct gag gtt gag atg att tgt gat gaa tac ggc 925
 Ser Ser His Leu Leu Ser Glu Val Glu Met Ile Cys Asp Glu Tyr Gly
 195 200 205
 gtc atg aaa aac gga gaa ctc ctg caa att aag agc aat cac cgc gat 973
 Val Met Lys Asn Gly Glu Leu Leu Gln Ile Lys Ser Asn His Arg Asp
 210 215 220
 acc gat acg gtt cgt tat cgg ctt aca tta aac ggc cac gcc gat gaa 1021

10294.000.ST25.txt

Thr	Asp	Thr	Val	Arg	Tyr	Arg	Leu	Thr	Leu	Asn	Gly	His	Ala	Asp	Glu	
		225					230					235				
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Ala	Ala	Asp	Leu	Leu	Asn	Glu	Tyr	Gln	Tyr	Ala	Gly	Gly	Leu	Thr	Glu	
	240					245					250					
gat	aaa	aat	gag	att	tat	gtc	ctt	tgc	atg	gaa	gaa	gac	att	atg	aaa	1117
Asp	Lys	Asn	Glu	Ile	Tyr	Val	Leu	Cys	Met	Glu	Glu	Asp	Ile	Met	Lys	
255					260					265					270	
gtc	gtt	aat	ctg	tta	atg	gag	aac	aaa	ata	aga	gtt	ctg	cat	atg	aag	1165
Val	Val	Asn	Leu	Leu	Met	Glu	Asn	Lys	Ile	Arg	Val	Leu	His	Met	Lys	
				275					280					285		
cag	gaa	aaa	cag	tcg	ata	gaa	caa	agc	ttt	ctg	gaa	ttg	atc	aat	aag	1213
Gln	Glu	Lys	Gln	Ser	Ile	Glu	Gln	Ser	Phe	Leu	Glu	Leu	Ile	Asn	Lys	
			290					295					300			
ggg	tta	ccg	gca	tta	ggg	tct	tga	aaaatgaact	ttacaggctg	atgggtgacga						1267
Gly	Leu	Pro	Ala	Leu	Gly	Ser										
		305														
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<210> 84

<211> 309

<212> PRT

<213> Bacillus licheniformis

<400> 84

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Thr Ile Phe Gly Leu Leu Gly Pro Asn Gly Ala Gly Lys Thr Thr Leu
35 40 45

Ile Lys Met Ile Val Gly Met Ala Lys Pro Thr Ser Gly Asp Ile Arg
50 55 60

Ile Asp Gly Tyr Ser Val Lys Ser Asn Tyr Glu Glu Ala Ala Ala Arg
65 70 75 80

Val Gly Ser Val Val Glu Asn Pro Ser Phe Tyr Glu His Leu Thr Gly
85 90 95

Tyr Gln Asn Leu Lys Tyr Leu Gly Gly Phe His Ser His Val Ser Lys
100 105 110

Glu Arg Ile Glu Glu Ile Val Gln Leu Val Asp Leu Thr Gly Ser Ile
115 120 125

His Lys Pro Val Lys Thr Tyr Ser Leu Gly Met Lys Gln Arg Leu Gly
130 135 140

Leu Ala Val Ala Leu Leu His Asp Pro Glu Phe Leu Ile Leu Asp Glu
145 150 155 160

Pro Thr Asn Gly Leu Asp Pro Gln Gly Ile Ile Asp Leu Arg Glu His
165 170 175

Leu Gln Tyr Leu Ala Lys Thr Phe Asn Lys Thr Ile Leu Ile Ser Ser
180 185 190

His Leu Leu Ser Glu Val Glu Met Ile Cys Asp Glu Tyr Gly Val Met
195 200 205

Lys Asn Gly Glu Leu Leu Gln Ile Lys Ser Asn His Arg Asp Thr Asp
210 215 220

Thr Val Arg Tyr Arg Leu Thr Leu Asn Gly His Ala Asp Glu Ala Ala
225 230 235 240

Asp Leu Leu Asn Glu Tyr Gln Tyr Ala Gly Gly Leu Thr Glu Asp Lys
245 250 255

Asn Glu Ile Tyr Val Leu Cys Met Glu Glu Asp Ile Met Lys Val Val
260 265 270

Asn Leu Leu Met Glu Asn Lys Ile Arg Val Leu His Met Lys Gln Glu
275 280 285

Lys Gln Ser Ile Glu Gln Ser Phe Leu Glu Leu Ile Asn Lys Gly Leu
290 295 300

Pro Ala Leu Gly Ser
305

<210> 85

<211> 1371

<212> DNA

<213> *Bacillus licheniformis*

<220>

<221> CDS

<222> (501)..(878)

<223>

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gggtgctttgt cggattcgct gtcattcacg taatcaaacc atacgagatc gtatttttga 180
atggattggg catctgcgac ctctgtgaa cggctctgaag cggatgatga acatcctgat 240
aagggaacgg ctaaaagcat cgcagccgcg gataaagaga tcagtttcga ttttttcact 300
gtgatcatcc tattcatttc ggtttcgctt ttatatacga acgatccggg caaagggtgc 360
atctattcaa aatagattgg cagaaaacag ggcgtaacaa ttgcatttta aacgtaaaca 420
aactgtaaaa taccatttct atgaaaaaag gtataatttg aatgtcagaa aaaaatccca 480
ttcacggagg atatttttat atg aag aag ata ctt ttt tct gtt ttt gtt ttg 533
Met Lys Lys Ile Leu Phe Ser Val Phe Val Leu
1 5 10

gca ggc agc ttg cta ttg gct ttt aat ttt gcc ggt gaa gcg agt gct 581
Ala Gly Ser Leu Leu Leu Ala Phe Asn Phe Ala Gly Glu Ala Ser Ala
15 20 25

aaa acg aaa aaa gtc agc ggc tat atc act tgg tac aac gga gtg ggc 629
Lys Thr Lys Lys Val Ser Gly Tyr Ile Thr Trp Tyr Asn Gly Val Gly
30 35 40

aaa atc ggc gct gac ggc aag agg ctc ggc cat tgg gac tgc gcc aca 677
Lys Ile Gly Ala Asp Gly Lys Arg Leu Gly His Trp Asp Cys Ala Thr
45 50 55

aag atg ggc ttc gat gtt ccg aga aaa ggc aca aaa ata aga gcc tat 725
Lys Met Gly Phe Asp Val Pro Arg Lys Gly Thr Lys Ile Arg Ala Tyr
60 65 70 75

tca aaa gca aaa ccg cac aaa gtc att aca gtc tat aaa tat gat gtc 773
Ser Lys Ala Lys Pro His Lys Val Ile Thr Val Tyr Lys Tyr Asp Val
80 85 90

ggc aga atg ccg ggc gct gtt ttg gat gta agc ccg aaa gct ttt aga 821
Gly Arg Met Pro Gly Ala Val Leu Asp Val Ser Pro Lys Ala Phe Arg
95 100 105

gct ttg gga ttt ccg aca agc aaa gga aag gta gcc gga cat tat aca 869
Ala Leu Gly Phe Pro Thr Ser Lys Gly Lys Val Ala Gly His Tyr Thr
110 115 120

tat aaa aaa taggagaaat gaagcaagaa aaatcgtttt cttgcttctt 918
Tyr Lys Lys
125

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gagcggcggt tcagacctgc ttgtatcgat aaccgatcag aagctgatga ccgcttacta 1098
tgaaaatcaa aataagctgt atgaagaaaa gatgacggat tatccggcta tggcattaga 1158
ccggaaaaaa cgaattcttt actatacaaa caccgataac agcaatgtga agcatttgat 1218
caggctggat ttacagtcgg gcaaaaaaac aaccctatat tcaggagatg aatatgtcga 1278
cgggctcagt ttatcggcgg acggttcgaa gctgttcatg agatacaacc ttgcggagga 1338
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<210> 86

<211> 126

<212> PRT

<213> Bacillus licheniformis

<400> 86

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20 25 30

Ser Gly Tyr Ile Thr Trp Tyr Asn Gly Val Gly Lys Ile Gly Ala Asp
35 40 45

Gly Lys Arg Leu Gly His Trp Asp Cys Ala Thr Lys Met Gly Phe Asp
50 55 60

Val Pro Arg Lys Gly Thr Lys Ile Arg Ala Tyr Ser Lys Ala Lys Pro
65 70 75 80

His Lys Val Ile Thr Val Tyr Lys Tyr Asp Val Gly Arg Met Pro Gly
85 90 95

Ala Val Leu Asp Val Ser Pro Lys Ala Phe Arg Ala Leu Gly Phe Pro
100 105 110

Thr Ser Lys Gly Lys Val Ala Gly His Tyr Thr Tyr Lys Lys
115 120 125

<210> 87

<211> 1957

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1454)

<223>

<400> 87
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 cttcgatatg tgtttgatca aatgtgccgg ggactgtcca tcagcccgaa gcttgctttt 180
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 cgttctgaga ggacgatcgg tctcgccgtc ctgaaagacc attatttgtc gccggcggca 360
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 Met Thr Lys Lys Gln Tyr Ser Tyr Ile Phe Thr
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 Leu Leu Leu Ala Phe Ala Val Phe Leu Ser Gly Cys Gln Ser Gly Gln
 15 20 25
 aaa cag gct gca tca gag aaa aat gaa gag aaa aca aga gtg gtg aaa 629
 Lys Gln Ala Ala Ser Glu Lys Asn Glu Glu Lys Thr Arg Val Val Lys
 30 35 40
 acc atc aac gga aat gtc act gta ccg gct aat ccg aag cgc gtc gtg 677
 Thr Ile Asn Gly Asn Val Thr Val Pro Ala Asn Pro Lys Arg Val Val
 45 50 55
 acg att ggc tat gcg gga acc atg ctt gca ttc ggg atc aag ccg ctt 725
 Thr Ile Gly Tyr Ala Gly Thr Met Leu Ala Phe Gly Ile Lys Pro Leu
 60 65 70 75
 gga gaa acg gga aag tac ctc gga agt cct tat att aaa gat caa gtt 773
 Gly Glu Thr Gly Lys Tyr Leu Gly Ser Pro Tyr Ile Lys Asp Gln Val
 80 85 90
 tca gga ata aag gat atc ggg gga aaa gac ggt ttt tca gta tct gtg 821
 Ser Gly Ile Lys Asp Ile Gly Gly Lys Asp Gly Phe Ser Val Ser Val
 95 100 105
 gaa aaa gtt ctt gaa ctt aaa ccc gat tta atc gta tcg atg acg aac 869
 Glu Lys Val Leu Glu Leu Lys Pro Asp Leu Ile Val Ser Met Thr Asn
 110 115 120
 gat tca aaa gaa tat gaa aag ctg tca aaa atc gct ccc act gtc gtc 917
 Asp Ser Lys Glu Tyr Glu Lys Leu Ser Lys Ile Ala Pro Thr Val Val
 125 130 135
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Tyr 140 Pro Phe Gly Thr Phe 145 Lys Asp Ala Arg Asp 150 Glu Met Lys Thr Phe 155
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 Gly Lys Leu Leu Gly Lys Glu Lys Glu Ala Arg Glu Trp Thr Lys Thr 170
 ttt aat caa aaa atg aaa gcc gcc cgc gcg aaa att aaa gat gca tct 1061
 Phe Asn Gln Lys Met Lys Ala Ala Arg Ala Lys Ile Lys Asp Ala Ser 185
 gta aaa ggt gaa acg ttc tct tta atc ggc gca tat gca aaa tct tta 1109
 Val Lys Gly Glu Thr Phe Ser Leu Ile Gly Ala Tyr Ala Lys Ser Leu 200
 tat gtc tac ggg gca tac ggg tat cgg ggc gga gaa gcg atc tat acg 1157
 Tyr Val Tyr Gly Ala Tyr Gly Tyr Arg Gly Gly Glu Ala Ile Tyr Thr 215
 cag ctg gga ctg acg ccg cct gaa tct gtt aaa aag gat gcc att gat 1205
 Gln Leu Gly Leu Thr Pro Pro Glu Ser Val Lys Lys Asp Ala Ile Asp 235
 aca gct gac gga tat aaa gcc ata tct ttc gag gtc ctg ccg aaa tat 1253
 Thr Ala Asp Gly Tyr Lys Ala Ile Ser Phe Glu Val Leu Pro Lys Tyr 250
 gcc gga gac tac ata ttt gtc gac gaa tca tac aac gga aag ctt gat 1301
 Ala Gly Asp Tyr Ile Phe Val Asp Glu Ser Tyr Asn Gly Lys Leu Asp 265
 cag gac aat ccg gtt tgg gca tcg ctt gac gcg gtg aaa aaa ggc aag 1349
 Gln Asp Asn Pro Val Trp Ala Ser Leu Asp Ala Val Lys Lys Gly Lys 280
 gtc ttt ttc ctc gat ccg gac aga ttt tgg ccg tat gat cca aac gct 1397
 Val Phe Phe Leu Asp Pro Asp Arg Phe Trp Pro Tyr Asp Pro Asn Ala 295
 gtt cag gca cag gcc gaa gaa atc gcc gac atg att tcc aag aaa gcg 1445
 Val Gln Ala Gln Ala Glu Glu Ile Ala Asp Met Ile Ser Lys Lys Ala 315
 aaa aat aaa tagaaaagcg gggagccgaa aagaatgatc cggttcccg 1494
 Lys Asn Lys
) ctttttcatt ttccataatg ctgaaattga atatccagtg tccggaggta cgtttgcagg 1554
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 ggaggcacga tgccgaacat tgcccacaat acatgggtga tcgtcagcgt ttgatcgaat 1854
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<210> 88

<211> 318

<212> PRT

<213> Bacillus licheniformis

<400> 88

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 35 40 45
 Val Thr Val Pro Ala Asn Pro Lys Arg Val Val Thr Ile Gly Tyr Ala
 50 55 60
 Gly Thr Met Leu Ala Phe Gly Ile Lys Pro Leu Gly Glu Thr Gly Lys
 65 70 75 80
 Tyr Leu Gly Ser Pro Tyr Ile Lys Asp Gln Val Ser Gly Ile Lys Asp
 85 90 95
 Ile Gly Gly Lys Asp Gly Phe Ser Val ser Val Glu Lys Val Leu Glu
 100 105 110
 Leu Lys Pro Asp Leu Ile Val Ser Met Thr Asn Asp Ser Lys Glu Tyr
 115 120 125
 Glu Lys Leu Ser Lys Ile Ala Pro Thr Val Val Tyr Pro Phe Gly Thr
 130 135 140
 Phe Lys Asp Ala Arg Asp Glu Met Lys Thr Phe Gly Lys Leu Leu Gly
 145 150 155 160
 Lys Glu Lys Glu Ala Arg Glu Trp Thr Lys Thr Phe Asn Gln Lys Met
 165 170 175
 Lys Ala Ala Arg Ala Lys Ile Lys Asp Ala Ser Val Lys Gly Glu Thr
 180 185 190
 Phe ser Leu Ile Gly Ala Tyr Ala Lys ser Leu Tyr Val Tyr Gly Ala
 195 200 205
 Tyr Gly Tyr Arg Gly Gly Glu Ala Ile Tyr Thr Gln Leu Gly Leu Thr
 210 215 220
 Pro Pro Glu Ser Val Lys Lys Asp Ala Ile Asp Thr Ala Asp Gly Tyr
 225 230 235 240

[illegible]

10294.000.ST25.txt

gaa gtg gtc gaa tct tca gtt gaa gtc gcc gaa atc acg aca aac ttg 677
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 aaa tca gac aat gta gtc cgt ttg tca atc aag ctt gaa acc gat tcg 725
 Lys Ser Asp Asn Val Val Arg Leu Ser Ile Lys Leu Glu Thr Asp Ser
 60 65 70 75
 aaa gag gcg aaa gaa gag ctt gaa aag cgg gat ttc caa att aaa gat 773
 Lys Glu Ala Lys Glu Glu Leu Glu Lys Arg Asp Phe Gln Ile Lys Asp
 80 85 90
 tca gtc atc tcc ctt ttg gcg aac acg aac gca gat gag ctt gaa gga 821
 Ser Val Ile Ser Leu Leu Ala Asn Thr Asn Ala Asp Glu Leu Glu Gly
 95 100 105
 caa aaa gga aaa gaa aaa ttt aaa gaa cag ctg aaa gaa aag ctg aac 869
 Gln Lys Gly Lys Glu Lys Phe Lys Glu Gln Leu Lys Glu Lys Leu Asn
 110 115 120
 acg aac tac atg aaa gag gga aaa gtg aaa act gtg tac att acc tcc 917
 Thr Asn Tyr Met Lys Glu Gly Lys Val Lys Thr Val Tyr Ile Thr Ser
 125 130 135
 ttt aat ctg cag taggaacata gatgacagaa ccatggaggt gaaaacagat 969
 Phe Asn Leu Gln
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 cccgaccatc gcctatacga tgatggaccg ggtgatgggc gggatcggct cgagccacaa 1389
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<210> 90

<211> 143

<212> PRT

<213> Bacillus licheniformis

<400> 90

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 20 25 30

Glu Lys Asp Gln Asn Ala Glu Pro Ser Ile Asp Glu Val Val Glu Ser
 35 40 45

10294.000.ST25.txt

Ser Val Glu Val Ala Glu Ile Thr Thr Asn Leu Lys Ser Asp Asn Val
50 55 60
Val Arg Leu Ser Ile Lys Leu Glu Thr Asp Ser Lys Glu Ala Lys Glu
65 70 75 80
Glu Leu Glu Lys Arg Asp Phe Gln Ile Lys Asp Ser Val Ile Ser Leu
85 90 95
Leu Ala Asn Thr Asn Ala Asp Glu Leu Glu Gly Gln Lys Gly Lys Glu
100 105 110
Lys Phe Lys Glu Gln Leu Lys Glu Lys Leu Asn Thr Asn Tyr Met Lys
115 120 125
Glu Gly Lys Val Lys Thr Val Tyr Ile Thr Ser Phe Asn Leu Gln
130 135 140

<210> 91
<211> 1366
<212> DNA
<213> Bacillus licheniformis

<220>
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<222> (488)..(874)
<223>

<400> 91
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cagaatgaat gtcggatgtt cgctctctgt tgtaaaagac ggactccgac gtctgaagac 180
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aatcagccgg aatacagcga tcgcatgat aaagaaaacg gccagcgtaa taaaagaagg 360
gatatatctt cttttgtctt caggaaaata gagcataaac tgaatcagaa acggcgccat 420
ttttcttcct ccctgaaatg atttttttac catttattta ttatgatacc attaggaggc 480
agatgca gtg aac aac caa ttt caa gtc gga gat cgc gta aag ggc ttt 529
Val Asn Asn Gln Phe Gln Val Gly Asp Arg Val Lys Gly Phe
1 5 10
tat aaa aca ggc gtc tac atc ggc gaa att acg gat gtt aaa ccg atg 577

10294.000.ST25.txt

Tyr Lys Thr Gly Val Tyr Ile Gly Glu Ile Thr Asp Val Lys Pro Met
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 His Tyr Leu Val Lys Ile Leu Ala Val Leu Thr His Pro Lys Gln Gly
 35 40 45
 gac ctt cat cat ccc aat cgg gca gac gtc cct ttt ttt cat gaa cga 673
 Asp Leu His His Pro Asn Arg Ala Asp Val Pro Phe Phe His Glu Arg
 50 55 60
 aaa gcg ctc gct tac ggt gaa cag acg aat atc ccg cac cgc atg gtg 721
 Lys Ala Leu Ala Tyr Gly Glu Gln Thr Asn Ile Pro His Arg Met Val
 65 70 75
 aag ccg ttc gat gaa gct gta ccg gat tat gcg gat tcg ctc cgc tca 769
 Lys Pro Phe Asp Glu Ala Val Pro Asp Tyr Ala Asp Ser Leu Arg Ser
 80 85 90
 gct ttg agc cgc tta aaa acg gat ctg caa aac gat tcg tcc gaa tac 817
 Ala Leu Ser Arg Leu Lys Thr Asp Leu Gln Asn Asp Ser Ser Glu Tyr
 95 100 105 110
 gcg gca aaa tcg ctt gag ctt att cat ggg ctt gaa aaa gaa tat ttc 865
 Ala Ala Lys Ser Leu Glu Leu Ile His Gly Leu Glu Lys Glu Tyr Phe
 115 120 125
 ctg cac aaa taacccaatc tgtttgcag attgggtttt ttatgtggcg 914
 Leu His Lys
 tgccgaaaga cttttgagag gtcaacccgt tcgccgatcg tcgtcggctt cggattttcc 974
 aaatacttct tatcccgttc tacgagccga aacaacttat acgttgtcat cgcgtcgtca 1034
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 <210> 92
 <211> 129
 <212> PRT
 <213> Bacillus licheniformis
 <400> 92
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 20 25 30

Leu Val Lys Ile Leu Ala Val Leu Thr His Pro Lys Gln Gly Asp Leu
 35 40 45

His His Pro Asn Arg Ala Asp Val Pro Phe Phe His Glu Arg Lys Ala
 50 55 60

Leu Ala Tyr Gly Glu Gln Thr Asn Ile Pro His Arg Met Val Lys Pro
 65 70 75 80

Phe Asp Glu Ala Val Pro Asp Tyr Ala Asp Ser Leu Arg Ser Ala Leu
 85 90 95

Ser Arg Leu Lys Thr Asp Leu Gln Asn Asp Ser Ser Glu Tyr Ala Ala
 100 105 110

Lys Ser Leu Glu Leu Ile His Gly Leu Glu Lys Glu Tyr Phe Leu His
 115 120 125

Lys

<210> 93

<211> 1909

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1406)

<223>

<400> 93
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 ctgaaaacgg agaaagcatg gagatccgcg gccgcgatct tttaacaggc ctgccgaaaa 180
 cgattgaaat cactgaaaaa gaaattacag cggctcttcg cgacactgtg accgccattg 240
 tcgatgccgt aaaaaatacg cttgaaaaaa ctccgcctga actcgcggct gatattatgg 300
 accgcggaat cgtccttacg ggaggcggcg cactgctgcg ccacctggac aaagtcatca 360
 gcgaagaaac gaaaatgccg gttttaattg cggaagaccc tcttgactgt gtagcgatcg 420
 gaacaggcaa agctctcgag caaattcatc tatttaaagg caaaaattaa ggacacaggg 480
 aatagaagag gtgtataatc atg ccg cag ttt ttt aca aat aaa cgg ttg atg 533
 Met Pro Gln Phe Phe Thr Asn Lys Arg Leu Met
 1 5 10

10294.000.ST25.txt

ctt tta ctc ctt tgt atc atc att tta gtg gca atg att gga ttt tcg Leu Leu Leu 15 Leu Cys Ile Ile Ile Leu 20 Val Ala Met Ile 25 Gly Phe Ser	581
tta aag aat gac cgg aat gca act tgg ccc gaa aaa ttt att ggc gat Leu Lys Asn 30 Asp Arg Asn Ala Thr 35 Trp Pro Glu Lys 40 Phe Ile Gly Asp	629
aca act ggt gta ttc cag acg att ttt cat acg ccc gct caa ttt ttt Thr Thr 45 Gly Val Phe Gln Thr 50 Ile Phe His Thr 55 Pro Ala Gln Phe Phe	677
gcg ggc ttc ttt gaa aat atc gaa gac tta aaa aat acg tac agc gaa Ala Gly Phe Phe Glu Asn 65 Ile Glu Asp Leu Lys 70 Asn Thr Tyr Ser Glu 75	725
aat gag cgc ctg cgg aaa aag ctc gac ggc cag aca caa tac gag gca Asn Glu Arg Leu 80 Arg Lys Lys Leu Asp Gly 85 Gln Thr Gln Tyr Glu Ala	773
aag ctg cag gag ctt gaa aat gaa aat aag tct tta aga aaa gag ctc Lys Leu Gln 95 Glu Leu Glu Asn Glu 100 Asn Lys Ser Leu Arg Lys 105 Glu Leu	821
ggc cat ctg aaa tca att aaa gac tac acg ccg att ctg gcg acc gtt Gly His 110 Leu Lys Ser Ile Lys Asp 115 Tyr Thr Pro Ile Leu 120 Ala Thr Val	869
atc gcc aga aat ccc gat aag tat gag tgg tgg aac ctg att acg atc Ile Ala Arg Asn Pro Asp Lys 130 Tyr Glu Trp Trp Asn 135 Leu Ile Thr Ile	917
aac aaa ggt tca aag cac ggc gtt gag aag gat atg gcg gta aca gat Asn Lys Gly Ser Lys 145 His Gly Val Glu Lys Asp 150 Met Ala Val Thr Asp 155	965
gaa aac ggc aac ttg atc gga aaa atc aaa agc aca aaa gtg aac aat Glu Asn Gly Asn 160 Leu Ile Gly Lys Ile Lys 165 Ser Thr Lys Val Asn Asn 170	1013
ttc act tcc acc gtc cag ctt tta agc gca aca gac aga aac aac aga Phe Thr Ser Thr 175 Val Gln Leu Leu Ser 180 Ala Thr Asp Arg 185 Asn Asn Arg	1061
atc tcc aca gtt atc gct gca gat aaa ggc aag aaa acg gtg aac gga Ile Ser Thr 190 Val Ile Ala Ala Asp 195 Lys Gly Lys Lys Thr 200 Val Asn Gly	1109
atc atc aac ggc tac gac tca gat aaa aag gcg ctt tcc atg gaa atc Ile Ile Asn Gly Tyr Asp Ser 210 Lys Lys Ala Leu 215 Ser Met Glu Ile	1157
atc gag cct gat gaa gac agg gaa gtg aaa aaa ggt gac ctc gtc gaa Ile Glu Pro Asp Glu Asp 225 Arg Glu Val Lys Lys 230 Gly Asp Leu Val Glu 235	1205
act tcc ggt gcg ggc ggc gtt ttt cct aaa ggc ctg aca atc gga aaa Thr Ser Gly Ala 240 Gly Gly Val Phe Pro Lys 245 Gly Leu Thr Ile Gly Lys 250	1253
gtg aca gag gtt gaa cca gat tcc tac ggt ttg acg aaa atc gct tat Val Thr Glu Val 255 Glu Pro Asp Ser Tyr 260 Gly Leu Thr Lys 265 Ile Ala Tyr	1301
gta gag ccg gca gcc gat atg tat aac ctt gat aac gtc atc gtc gtc Val Glu Pro 270 Ala Ala Asp Met Tyr 275 Asn Leu Asp Asn Val 280 Ile Val Val	1349

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gac aga acg ctt gat acg gtg gat gtc gac aag atg gac gat gag gag 1397
 Asp Arg Thr Leu Asp Thr Val Asp Val Asp Lys Met Asp Asp Glu Glu
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gaa ggg tcg tgaaacgctt cttcttcccc gtcgtcatga tgtttgtttt 1446
 Glu Gly Ser
 300

agtatctgac agcgtctatg cggattttgt caacttgcct tttgtgacgg aagaacagca 1506
 gctcatcccg cgttttctgc tgcttgcttt agtttttatg acggcttatg tcaatcagcc 1566
 ttttgccatt acatatggat ttattttcgg actgttatat gatattaatt acaccgacct 1626
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 agtattgcag acaaacgcgc tggctgcat ttttatttcg ctgctcgccg tctgtgttct 1746
 tgaattttac caatatggcg tgcagatgct gatacgtccg gaaattatgc cgttccatca 1806
 atttgtgctc ggcaggctcc tgcccacgct tgcgtgaac gccgttgggc gccttctgct 1866
 catttacccg ttcaaattggg tttttaccag tcttaagaaa gag 1909

<210> 94

<211> 302

<212> PRT

<213> Bacillus licheniformis

<400> 94

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 20 25 30

Asn Ala Thr Trp Pro Glu Lys Phe Ile Gly Asp Thr Thr Gly Val Phe
 35 40 45

Gln Thr Ile Phe His Thr Pro Ala Gln Phe Phe Ala Gly Phe Phe Glu
 50 55 60

Asn Ile Glu Asp Leu Lys Asn Thr Tyr Ser Glu Asn Glu Arg Leu Arg
 65 70 75 80

Lys Lys Leu Asp Gly Gln Thr Gln Tyr Glu Ala Lys Leu Gln Glu Leu
 85 90 95

Glu Asn Glu Asn Lys Ser Leu Arg Lys Glu Leu Gly His Leu Lys Ser
 100 105 110

Ile Lys Asp Tyr Thr Pro Ile Leu Ala Thr Val Ile Ala Arg Asn Pro
 115 120 125

10294.000.ST25.txt

Asp Lys Tyr Glu Trp Trp Asn Leu Ile Thr Ile Asn Lys Gly Ser Lys
 130 135 140
 His Gly Val Glu Lys Asp Met Ala Val Thr Asp Glu Asn Gly Asn Leu
 145 150 155 160
 Ile Gly Lys Ile Lys Ser Thr Lys Val Asn Asn Phe Thr Ser Thr Val
 165 170 175
 Gln Leu Leu Ser Ala Thr Asp Arg Asn Asn Arg Ile Ser Thr Val Ile
 180 185 190
 Ala Ala Asp Lys Gly Lys Lys Thr Val Asn Gly Ile Ile Asn Gly Tyr
 195 200 205
 Asp Ser Asp Lys Lys Ala Leu Ser Met Glu Ile Ile Glu Pro Asp Glu
 210 215 220
 Asp Arg Glu Val Lys Lys Gly Asp Leu Val Glu Thr Ser Gly Ala Gly
 225 230 235 240
 Gly Val Phe Pro Lys Gly Leu Thr Ile Gly Lys Val Thr Glu Val Glu
 245 250 255
 Pro Asp Ser Tyr Gly Leu Thr Lys Ile Ala Tyr Val Glu Pro Ala Ala
 260 265 270
 Asp Met Tyr Asn Leu Asp Asn Val Ile Val Val Asp Arg Thr Leu Asp
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<210> 95

<211> 1450

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (121)..(951)

<223>

<400> 95
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60

10294.000.ST25.txt

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caa agg gtg ctc acc cac ctg aaa agc ctg cct gaa gag ctg ttc acc Gln Arg Val Leu Thr His Leu Lys Ser Leu Pro Glu Glu Leu Phe Thr 20 25 30	216
cgg gaa atc aaa agc gtt ttt caa act gta tct gag gtt gtt acc cat Arg Glu Ile Lys Ser Val Phe Gln Thr Val Ser Glu Val Val Thr His 35 40 45	264
atg tgc ggc gct gac gac ctt agg ctg aaa gat acc acc ctc tta acc Met Cys Gly Ala Asp Asp Leu Arg Leu Lys Asp Thr Thr Leu Leu Thr 50 55 60	312
aga aag tgt ggg gga aag tat acc cgc aga acc gtt caa aaa atg aag Arg Lys Cys Gly Gly Lys Tyr Thr Arg Arg Thr Val Gln Lys Met Lys 65 70 75 80	360
cca aag ttt agg ttg cag tgt cag ttt aag aag aag cgc caa aag tac Pro Lys Phe Arg Leu Gln Cys Gln Phe Lys Lys Lys Arg Gln Lys Tyr 85 90 95	408
att tgt ggt gaa agg aat aat att ggg cgg aac act gtc aat ggt aat Ile Cys Gly Glu Arg Asn Asn Ile Gly Arg Asn Thr Val Asn Gly Asn 100 105 110	456
ttt aaa gca agc cga ttt aat gaa aaa tgg gta acc gac att acc tac Phe Lys Ala Ser Arg Phe Asn Glu Lys Trp Val Thr Asp Ile Thr Tyr 115 120 125	504
tta cat tat ggc tcc gat atg tta tat tta tca acg att atg gac tta Leu His Tyr Gly Ser Asp Met Leu Tyr Leu Ser Thr Ile Met Asp Leu 130 135 140	552
tat aac aac gaa ata gtg gct tac aaa ata ggt acg agc caa gat att Tyr Asn Asn Glu Ile Val Ala Tyr Lys Ile Gly Thr Ser Gln Asp Ile 145 150 155 160	600
aac cta gta tta gac aca ttg agg gaa gct gta gaa tta cgt aaa cca Asn Leu Val Leu Asp Thr Leu Arg Glu Ala Val Glu Leu Arg Lys Pro 165 170 175	648
gta ggg tta ctt ctt cat agc gac cag gga tct gtc tat act tca cat Val Gly Leu Leu Leu His Ser Asp Gln Gly Ser Val Tyr Thr Ser His 180 185 190	696
gca tat cag aat ttg gcc aaa gaa aaa ggc att acc aca agc atg tct Ala Tyr Gln Asn Leu Ala Lys Glu Lys Gly Ile Thr Thr Ser Met Ser 195 200 205	744
cga aaa gga aac tgc cat gat aat gcc gtc att gaa tcc ttt cac tcc Arg Lys Gly Asn Cys His Asp Asn Ala Val Ile Glu Ser Phe His Ser 210 215 220	792
tcg cta aag tcg gaa gga ttt aac gct caa agt aga gca tct ata tcc Ser Leu Lys Ser Glu Gly Phe Asn Ala Gln Ser Arg Ala Ser Ile Ser 225 230 235 240	840
aat tct aaa gta gta caa att gta aat caa tac atg tat cga tat aat Asn Ser Lys Val Val Gln Ile Val Asn Gln Tyr Met Tyr Arg Tyr Asn 245 250 255	888
cat gta cga att cag gca aaa tta aac tac ctg tcc cca ctg gaa tac	936

His Val Arg Ile Gln Ala Lys Leu Asn Tyr Leu Ser Pro Leu Glu Tyr
 260 265 270

agg gga cag gca gca taggtgtttt ttctaagtct cattttaacg ggtcagttca 991
 Arg Gly Gln Ala Ala
 275

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<211> 277

<212> PRT

<213> Bacillus licheniformis

<400> 96

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 20 25 30

Arg Glu Ile Lys Ser Val Phe Gln Thr Val Ser Glu Val Val Thr His
 35 40 45

Met Cys Gly Ala Asp Asp Leu Arg Leu Lys Asp Thr Thr Leu Leu Thr
 50 55 60

Arg Lys Cys Gly Gly Lys Tyr Thr Arg Arg Thr Val Gln Lys Met Lys
 65 70 75 80

Pro Lys Phe Arg Leu Gln Cys Gln Phe Lys Lys Lys Arg Gln Lys Tyr
 85 90 95

Ile Cys Gly Glu Arg Asn Asn Ile Gly Arg Asn Thr Val Asn Gly Asn
 100 105 110

Phe Lys Ala Ser Arg Phe Asn Glu Lys Trp Val Thr Asp Ile Thr Tyr
 115 120 125

10294.000.ST25.txt

Leu His Tyr Gly Ser Asp Met Leu Tyr Leu Ser Thr Ile Met Asp Leu
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Tyr Asn Asn Glu Ile Val Ala Tyr Lys Ile Gly Thr Ser Gln Asp Ile
145 150 155 160

Asn Leu Val Leu Asp Thr Leu Arg Glu Ala Val Glu Leu Arg Lys Pro
165 170 175

Val Gly Leu Leu Leu His Ser Asp Gln Gly Ser Val Tyr Thr Ser His
180 185 190

Ala Tyr Gln Asn Leu Ala Lys Glu Lys Gly Ile Thr Thr Ser Met Ser
195 200 205

Arg Lys Gly Asn Cys His Asp Asn Ala Val Ile Glu Ser Phe His Ser
210 215 220

Ser Leu Lys Ser Glu Gly Phe Asn Ala Gln Ser Arg Ala Ser Ile Ser
225 230 235 240

Asn Ser Lys Val Val Gln Ile Val Asn Gln Tyr Met Tyr Arg Tyr Asn
245 250 255

His Val Arg Ile Gln Ala Lys Leu Asn Tyr Leu Ser Pro Leu Glu Tyr
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Arg Gly Gln Ala Ala
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<210> 97

<211> 2312

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1925)

<223>

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cttaaacagg acaagagcga atcggttaaat aaggaaatca tgaggctcta ctttaacggg 180
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gtctccgccg aggatatcgg gattatcacg atccaggagc aagggttcatt cgttgaaatt 300
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tttgctcgta ataaaccttg gataagcagc atatgatgga ttgtcaaaaa atgaaagcgt 480
tttaaaagag aggagaacaa atg aat atg aga aag tgt ttc atc caa gtc ctt 533
                        Met Asn Met Arg Lys Cys Phe Ile Gln Val Leu
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gca ttg ctt ttc atc att gct gca tgt ttc gcg cca aac caa gcc tct 581
Ala Leu Leu Phe Ile Ile Ala Ala Cys Phe Ala Pro Asn Gln Ala Ser
                        15          20          25

gca caa act caa aaa cct gtt ttt tca gaa gtg acg gta cat gat cca 629
Ala Gln Thr Gln Lys Pro Val Phe Ser Glu Val Thr Val His Asp Pro
                        30          35          40

tcg att att aaa gcg aat ggc acg tac tat gtc ttc ggc tcc cat tta 677
Ser Ile Ile Lys Ala Asn Gly Thr Tyr Tyr Val Phe Gly Ser His Leu
                        45          50          55

gct tcg gcc aaa tcg acg gac ctg atg aat tgg acg caa att tcc tcg 725
Ala Ser Ala Lys Ser Thr Asp Leu Met Asn Trp Thr Thr Gln Ile Ser Ser
60          65          70          75

agt gtc cac gac ggc aat cct ctg att ccg aac gtc tat gaa gaa tta 773
Ser Val His Asp Gly Asn Pro Leu Ile Pro Asn Val Tyr Glu Glu Leu
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aaa gaa acc ttt gaa tgg gct gaa tct gat acg ttg tgg gca cct gat 821
Lys Glu Thr Phe Glu Trp Ala Glu Ser 100 Asp Thr Leu Trp Ala Pro Asp
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gtc acc cag ctt gag gac ggc aag ttt tat atg tat tac aac gcc tgc 869
Val Thr Gln Leu Glu Asp Gly Lys Phe Tyr Met Tyr Tyr Asn Ala Cys
                        110          115          120

cgc ggg gat tct ccg aga tcc gcc ctc ggg ctt gct gtc gca gac gac 917
Arg Gly Asp Ser Pro Arg Ser Ala Leu Gly Leu Ala Val Ala Asp Asp
125          130          135

att gaa ggt cca tac aaa aat aaa ggc att ttt ctg aag tcg gga atg 965
Ile Glu Gly Pro Tyr Lys Asn Lys Gly Ile Phe Leu Lys Ser Gly Met
140          145          150          155

gat ggg atc agc aat gac ggg acg cct tat gac gcg aca aag cac cca 1013
Asp Gly Ile Ser Asn 160 Asp Gly Thr Pro Tyr Asp Ala Thr Lys His Pro
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aat gtc gtc gat ccc cac aca ttc ttt gat caa aac gga aag ctg tgg 1061
Asn Val Val Asp Pro His Thr Phe Phe Asp Gln Asn Gly Lys Leu Trp
175          180          185

atg gtg tac ggc tcc tat tcc ggc gga att ttt att tta gaa atg gac 1109
Met Val Tyr Gly Ser Tyr Ser Gly Gly Ile Phe Ile Leu Glu Met Asp
190          195          200

aag aaa acc gga ttt ccg ctt ccg gga cag gga tac ggc aaa aag ctg 1157
Lys Lys Thr Gly Phe Pro Leu Pro Gly Gln Gly Tyr Gly Lys Lys Leu
205          210          215

atc ggc ggc aac cac agc cgt att gaa ggc gca tat att ctc tac cat 1205
Ile Gly Gly Asn His Ser Arg Ile Glu Gly Ala Tyr Ile Leu Tyr His
220          225          230          235

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10294.000.ST25.txt

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gct Ala	gac Asp	ggg Gly	ggt Gly 255	tac Tyr	aac Asn	att Ile	cgc Arg	gtc Val 260	gcc Ala	cgc Arg	tcc Ser	aaa Lys	aac Asn 265	cct Pro	gac Asp	1301
ggg Gly	cct Pro	tat Tyr 270	tat Tyr	gat Asp	gca Ala	gaa Glu	ggc Gly 275	cac His	gcg Ala	atg Met	att Ile	gac Asp 280	gtc Val	cgc Arg	ggc Gly	1349
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aaa Lys 300	ctg Leu	atg Met	gga Gly	aat Asn	ttc Phe 305	tca Ser	ttt Phe	aac Asn	aat Asn	aaa Lys 310	aac Asn	ggc Gly	tat Tyr	gtg Val	tcg Ser 315	1445
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cgc Arg	gtc Val	cac His 350	caa Gln	ttg Leu	ctg Leu	atg Met	aac Asn 355	aaa Lys	caa Gln	ggc Gly	tgg Trp	ccg Pro 360	gtt Val	gtc Val	gcc Ala	1589
cct Pro	cac His 365	cgc Arg	tat Tyr	gcc Ala	gga Gly	gag Glu 370	aag Lys	ctt Leu	gaa Glu	aag Lys	gtg Val 375	aaa Lys	aag Lys	tca Ser	gat Asp	1637
gtg Val 380	att Ile	ggc Gly	gat Asp	tac Tyr	gaa Glu 385	ttg Leu	gtg Val	agg Arg	cac His	ggc Gly 390	aaa Lys	gac Asp	atc Ile	tcc Ser	gca Ala 395	1685
gat Asp	att Ile	aaa Lys	gaa Glu	tcg Ser 400	aaa Lys	gaa Glu	atc Ile	cgc Arg	ttg Leu 405	aat Asn	caa Gln	aat Asn	ggc Gly	aaa Lys 410	ata Ile	1733
aca Thr	ggc Gly	gca Ala	gta Val 415	gcc Ala	gga Gly	acg Thr	tgg Trp	aag Lys 420	aac Asn	acg Thr	ggg Gly	cat His	aac Asn 425	aaa Lys	ata Ile	1781
gaa Glu	ctc Leu	aag Lys 430	atc Ile	gac Asp	gga Gly	aaa Lys	acc Thr 435	tac Tyr	gat Asp	ggc Gly	gtg Val	ttt Phe 440	ttg Leu	cgt Arg	cag Gln	1829
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cgt Arg 460	gag Glu	gga Gly	gat Asp	gcg Ala	gtt Val 465	tgg Trp	ggg Gly	agt Ser	agt Ser	tta Leu 470	aaa Lys	aga Arg	gcg Ala	gaa Glu	ttt Phe 475	1925
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<211> 475

<212> PRT

<213> Bacillus licheniformis

<400> 98

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Pro Val Phe Ser Glu Val Thr Val His Asp Pro Ser Ile Ile Lys Ala
 35 40 45

Asn Gly Thr Tyr Tyr Val Phe Gly Ser His Leu Ala Ser Ala Lys Ser
 50 55 60

Thr Asp Leu Met Asn Trp Thr Gln Ile Ser Ser Ser Val His Asp Gly
 65 70 75 80

Asn Pro Leu Ile Pro Asn Val Tyr Glu Glu Leu Lys Glu Thr Phe Glu
 85 90 95

Trp Ala Glu Ser Asp Thr Leu Trp Ala Pro Asp Val Thr Gln Leu Glu
 100 105 110

Asp Gly Lys Phe Tyr Met Tyr Tyr Asn Ala Cys Arg Gly Asp Ser Pro
 115 120 125

Arg Ser Ala Leu Gly Leu Ala Val Ala Asp Asp Ile Glu Gly Pro Tyr
 130 135 140

Lys Asn Lys Gly Ile Phe Leu Lys Ser Gly Met Asp Gly Ile Ser Asn
 145 150 155 160

Asp Gly Thr Pro Tyr Asp Ala Thr Lys His Pro Asn Val Val Asp Pro
 165 170 175

His Thr Phe Phe Asp Gln Asn Gly Lys Leu Trp Met Val Tyr Gly Ser
 180 185 190

Tyr Ser Gly Gly Ile Phe Ile Leu Glu Met Asp Lys Lys Thr Gly Phe
 195 200 205
 Pro Leu Pro Gly Gln Gly Tyr Gly Lys Lys Leu Ile Gly Gly Asn His
 210 215 220
 Ser Arg Ile Glu Gly Ala Tyr Ile Leu Tyr His Pro Glu Thr Gln Tyr
 225 230 235 240
 Tyr Tyr Leu Tyr Met Ser Phe Gly Gly Leu Ala Ala Asp Gly Gly Tyr
 245 250 255
 Asn Ile Arg Val Ala Arg Ser Lys Asn Pro Asp Gly Pro Tyr Tyr Asp
 260 265 270
 Ala Glu Gly His Ala Met Ile Asp Val Arg Gly Lys Glu Gly Thr Leu
 275 280 285
 Phe Asp Asp Arg Ser Ile Glu Pro Tyr Gly Val Lys Leu Met Gly Asn
 290 295 300
 Phe Ser Phe Asn Asn Lys Asn Gly Tyr Val Ser Pro Gly His Asn Ser
 305 310 315 320
 Ala Phe Tyr Asp Glu Lys Ser Gly Lys Ser Tyr Leu Ile Phe His Thr
 325 330 335
 Arg Phe Pro Gly Arg Gly Glu Glu His Glu Val Arg Val His Gln Leu
 340 345 350
 Leu Met Asn Lys Gln Gly Trp Pro Val Val Ala Pro His Arg Tyr Ala
 355 360 365
 Gly Glu Lys Leu Glu Lys Val Lys Lys Ser Asp Val Ile Gly Asp Tyr
 370 375 380
 Glu Leu Val Arg His Gly Lys Asp Ile Ser Ala Asp Ile Lys Glu Ser
 385 390 395 400
 Lys Glu Ile Arg Leu Asn Gln Asn Gly Lys Ile Thr Gly Ala Val Ala
 405 410 415
 Gly Thr Trp Lys Asn Thr Gly His Asn Lys Ile Glu Leu Lys Ile Asp
 420 425 430
 Gly Lys Thr Tyr Asp Gly Val Phe Leu Arg Gln Trp Asp Ala Ala Ser
 435 440 445
 Glu Arg Lys Val Met Thr Phe Ser Ala Leu Ser Arg Glu Gly Asp Ala
 450 455 460

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<210> 99

<211> 1828

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1325)

<223>

<400> 99

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ttcattaaac ttctgtttt attaccgata ttag	gaaggg agttccttta tggatgatgaa	480
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	Met Lys Lys Ser Leu Phe Leu Phe Val Phe Ser	
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ttg ttt ttg atg gcg att cca gca ttt tcg	gct tcg gcg aat gtt tac	581
Leu Phe Leu Met Ala Ile Pro Ala Phe Ser	Ala Ser Ala Asn Val Tyr	
	15 20 25	
gaa gat gag tat gaa ccc aac aat tct ttc	gct gag gct tac gat gta	629
Glu Asp Glu Tyr Glu Pro Asn Asn Ser Phe	Ala Glu Ala Tyr Asp Val	
	30 35 40	
ggg ttg tgg aaa tac aag acg att tcg gcg	acg att cac agc gaa agc	677
Gly Leu Trp Lys Tyr Lys Thr Ile Ser Ala	Thr Ile His Ser Glu Ser	
	45 50 55	
gat aaa gat tat tac aaa ttt tac gcg aca	aag gga gaa cag ctt gcc	725
Asp Lys Asp Tyr Tyr Lys Phe Tyr Ala Thr	Lys Gly Glu Gln Leu Ala	
	60 65 70 75	
att cac cta aag aac atc ccg gca aat aca	gat tat gat cta tat tta	773
Ile His Leu Lys Asn Ile Pro Ala Asn Thr	Asp Tyr Asp Leu Tyr Leu	
	80 85 90	
ttt aaa gat gct tac ggc tat ccc gca gta	gga tct tct gaa aga atg	821
Phe Lys Asp Ala Tyr Gly Tyr Pro Ala Val	Gly Ser Ser Glu Arg Met	
	95 100 105	

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 tac att gcg gtc gtc atg tct aaa gac ggt tca tat gac ggc tgg gga 917
 Tyr Ile Ala Val Val Met Ser Lys Asp Gly Ser Tyr Asp Gly Trp Gly
 125 130 135
 ttt tac aga ctt gaa ttt atc gac aga atg aag agc ggt gct tat acg 965
 Phe Tyr Arg Leu Glu Phe Ile Asp Arg Met Lys Ser Gly Ala Tyr Thr
 140 145 150 155
 gcg aat ttg tct ccg tca tcc atc tca agc ccg gga cag gga gtc gtt 1013
 Ala Asn Leu Ser Pro Ser Ser Ile Ser Ser Pro Gly Gln Gly Val Val
 160 165 170
 tct ccg gtt gcc gcc gtc aat ctt gcc aat gcc tcg gcc att ccc gaa 1061
 Ser Pro Val Ala Ala Val Asn Leu Ala Asn Ala Ser Ala Ile Pro Glu
 175 180 185
 gga gcg act gtg aaa agc gtt tct gcc gag gga acg ata tat cca agt 1109
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 His Thr Ser Val Ser Gly Gly Thr Leu Phe Pro Asp Leu Lys Pro Glu
 220 225 230 235
 ctt gcg ctt ccc gtc aaa acg aca tgg aat gtg aga tac tat tcg ctc 1253
 Leu Ala Leu Pro Val Lys Thr Thr Trp Asn Val Arg Tyr Tyr Ser Leu
 240 245 250
 gct tgg agc agt tca act tgg aga tcg ccg cag ctg aag atc aat tat 1301
 Ala Trp Ser Ser Ser Thr Trp Arg Ser Pro Gln Leu Lys Ile Asn Tyr
 255 260 265
 caa tac gat tca aca tac ggc tgg taaacagatc caaatcccgg ccgatataaa 1355
 Gln Tyr Asp Ser Thr Tyr Gly Trp
 270 275
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 <211> 275
 <212> PRT

<213> Bacillus licheniformis

<400> 100

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 35 40 45

Lys Thr Ile Ser Ala Thr Ile His Ser Glu Ser Asp Lys Asp Tyr Tyr
 50 55 60

Lys Phe Tyr Ala Thr Lys Gly Glu Gln Leu Ala Ile His Leu Lys Asn
 65 70 75 80

Ile Pro Ala Asn Thr Asp Tyr Asp Leu Tyr Leu Phe Lys Asp Ala Tyr
 85 90 95

Gly Tyr Pro Ala Val Gly Ser Ser Glu Arg Met Gly Asn Gln Asn Glu
 100 105 110

Ile Ile Arg Leu Asp Val Pro Glu Thr Gly Arg Tyr Ile Ala Val Val
 115 120 125

Met Ser Lys Asp Gly Ser Tyr Asp Gly Trp Gly Phe Tyr Arg Leu Glu
 130 135 140

Phe Ile Asp Arg Met Lys Ser Gly Ala Tyr Thr Ala Asn Leu Ser Pro
 145 150 155 160

Ser Ser Ile Ser Ser Pro Gly Gln Gly Val Val Ser Pro Val Ala Ala
 165 170 175

Val Asn Leu Ala Asn Ala Ser Ala Ile Pro Glu Gly Ala Thr Val Lys
 180 185 190

Ser Val Ser Ala Glu Gly Thr Ile Tyr Pro Ser Leu Gly His Thr Tyr
 195 200 205

Arg Glu Val Leu Asn Lys Glu Glu Gly Val Trp His Thr Ser Val Ser
 210 215 220

Gly Gly Thr Leu Phe Pro Asp Leu Lys Pro Glu Leu Ala Leu Pro Val
 225 230 235 240

Lys Thr Thr Trp Asn Val Arg Tyr Tyr Ser Leu Ala Trp Ser Ser Ser
 245 250 255

10294.000.ST25.txt

Thr Trp Arg Ser Pro Gln Leu Lys Ile Asn Tyr Gln Tyr Asp Ser Thr
 260 265 270

Tyr Gly Trp
 275

<210> 101

<211> 2584

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (510)..(2081)

<223>

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 cttgcctact attctccatc ttcagttcag ctcatatgta cactaattta tattataata 180
 cgagtgttac gtttgcattg caaccctatt tgcgggttctt tttattctga attgattctt 240
 tggacgtcag cccagctca gtggccggtt cttccatgaa gccggcgcg cccgggtccg 300
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 Asn Met Lys Lys Arg Ala Val Leu
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 Ile Leu Ser Met Met Leu Ala Ala Gln Ala Ala Phe Tyr Thr Ser Ser
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 aac aca gct tct gca gcc atc ggg gaa gcc gtg att gcc acc gat gaa 629
 Asn Thr Ala Ser Ala Ala Ile Gly Glu Ala Val Ile Ala Thr Asp Glu
 25 30 35 40
 atc aat gtc aga agc ggg cct gga ctg agc cac gaa atc gtc agc gtc 677
 Ile Asn Val Arg Ser Gly Pro Gly Leu Ser His Glu Ile Val Ser Val
 45 50 55
 gtc agc agg aat gaa agc tat ccg att ctt gaa gaa cgc ggg gat tgg 725
 Val Ser Arg Asn Glu Ser Tyr Pro Ile Leu Glu Glu Arg Gly Asp Trp
 60 65 70
 gtg caa atc cag ctg aac ggc ggg caa aaa ggc tgg gtc gta tcc tgg 773

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Val	Gln	Ile	Gln	Leu	Asn	Gly	Gly	Gln	Lys	Gly	Trp	Val	Val	Ser	Trp	
75							80					85				
ctg	atc	aag	aaa	aag	agc	caa	gtc	tcc	agc	gga	tct	gat	tcc	gca	tcg	821
Leu	Ile	Lys	Lys	Lys	Ser	Gln	Val	Ser	Ser	Gly	Ser	Asp	Ser	Ala	Ser	
90						95					100					
gga	aaa	gtc	aca	tct	tcc	gaa	gca	aac	ttg	aga	atc	aga	aaa	ggc	ccc	869
Gly	Lys	Val	Thr	Ser	Ser	Glu	Ala	Asn	Leu	Arg	Ile	Arg	Lys	Gly	Pro	
105					110					115					120	
ggc	act	tca	tat	gaa	gtc	caa	ggc	gta	ttc	cct	gaa	gga	gaa	cag	gct	917
Gly	Thr	Ser	Tyr	Glu	Val	Gln	Gly	Val	Phe	Pro	Glu	Gly	Glu	Gln	Ala	
				125					130					135		
gac	ctg	cta	aag	acc	gac	gga	aaa	tgg	ata	aag	att	tcc	tat	cag	aac	965
Asp	Leu	Leu	Lys	Thr	Asp	Gly	Lys	Trp	Ile	Lys	Ile	Ser	Tyr	Gln	Asn	
			140					145					150			
atc	aca	ggc	tgg	gtc	tat	tca	gat	tat	gtc	aat	caa	ggt	tca	ggc	gcg	1013
Ile	Thr	Gly	Trp	Val	Tyr	Ser	Asp	Tyr	Val	Asn	Gln	Gly	Ser	Gly	Ala	
		155					160					165				
aaa	cag	tct	caa	tcg	tct	tca	tca	cat	gct	tca	tca	tca	aaa	tcg	gga	1061
Lys	Gln	Ser	Gln	Ser	Ser	Ser	Ser	His	Ala	Ser	Ser	Ser	Lys	Ser	Gly	
	170					175					180					
acg	gtc	ggc	gta	tcc	acc	tta	aat	gtc	agg	agc	aca	gct	tcc	cat	caa	1109
Thr	Val	Gly	Val	Ser	Thr	Leu	Asn	Val	Arg	Ser	Thr	Ala	Ser	His	Gln	
185					190				195						200	
ggc	cgg	att	att	gcc	acg	ctc	caa	cgg	aat	gca	agt	gtg	acg	att	tta	1157
Gly	Arg	Ile	Ile	Ala	Thr	Leu	Gln	Arg	Asn	Ala	Ser	Val	Thr	Ile	Leu	
				205					210					215		
aac	gaa	cag	cac	ggc	tgg	tat	gaa	atc	gaa	ttt	aat	gga	caa	aaa	ggc	1205
Asn	Glu	Gln	His	Gly	Trp	Tyr	Glu	Ile	Glu	Phe	Asn	Gly	Gln	Lys	Gly	
			220					225					230			
tgg	gcc	gca	agc	cac	tat	att	ctc	gaa	gga	aac	aaa	cag	aac	agc	gga	1253
Trp	Ala	Ala	Ser	His	Tyr	Ile	Leu	Glu	Gly	Asn	Lys	Gln	Asn	Ser	Gly	
		235					240						245			
acc	tcc	gga	aca	agc	agc	agc	tcc	gaa	gca	aaa	cgg	cag	ggc	acc	atc	1301
Thr	Ser	Gly	Thr	Ser	Ser	Ser	Ser	Glu	Ala	Lys	Arg	Gln	Gly	Thr	Ile	
	250					255					260					
gtg	tat	gaa	agc	aca	aat	gtt	aga	agc	ggg	gcc	tcg	aca	tcc	tca	gcg	1349
Val	Tyr	Glu	Ser	Thr	Asn	Val	Arg	Ser	Gly	Ala	Ser	Thr	Ser	Ser	Ala	
265					270				275						280	
atc	gtc	aaa	cgc	acg	gga	aaa	ggc	gag	tct	tac	ccg	atc	gtc	tct	aca	1397
Ile	Val	Lys	Arg	Thr	Gly	Lys	Gly	Glu	Ser	Tyr	Pro	Ile	Val	Ser	Thr	
				285					290					295		
aaa	gga	gac	tgg	tat	gaa	atc	aaa	ctg	tca	aac	ggc	gat	tcc	gct	tat	1445
Lys	Gly	Asp	Trp	Tyr	Glu	Ile	Lys	Leu	Ser	Asn	Gly	Asp	Ser	Ala	Tyr	
			300					305					310			
gtc	gca	agc	tgg	gtc	gtt	cag	act	gtt	gac	cag	gca	ggc	tca	gcc	gga	1493
Val	Ala	Ser	Trp	Val	Val	Gln	Thr	Val	Asp	Gln	Ala	Gly	Ser	Ala	Gly	
		315					320					325				
gat	tcg	aaa	agc	gca	gca	ccg	cct	ttg	gca	aag	cgg	tca	agc	tcg	gga	1541
Asp	Ser	Lys	Ser	Ala	Ala	Pro	Pro	Leu	Ala	Lys	Arg	Ser	Ser	Ser	Gly	
	330					335					340					
ggc	aca	atc	aaa	aat	aaa	acg	gtt	gtc	atc	gat	gcc	gga	cat	gga	gga	1589

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Gly Thr Ile Lys Asn Lys Thr Val Val Ile Asp Ala Gly His Gly Gly
 345 350 355 360
 cat gac agc ggg aca atc gga acg cgg ggg acg ctc gaa aaa cgg ctg 1637
 His Asp Ser Gly Thr Ile Gly Thr Arg Gly Thr Leu Glu Lys Arg Leu
 365 370 375
 acc atc aaa acg gca acg ctt ctt gcc gcg aaa ctc aga gcc gat ggc 1685
 Thr Ile Lys Thr Ala Thr Leu Leu Ala Ala Lys Leu Arg Ala Asp Gly
 380 385 390
 gtc aac gtc tat atg acg cgg aat gac gat tct ttc gtc agc ctt cag 1733
 Val Asn Val Tyr Met Thr Arg Asn Asp Asp Ser Phe Val Ser Leu Gln
 395 400 405
 tcg cgg gtc gcg acc tct cat tac cga aac gcc gac gct ttt atc agc 1781
 Ser Arg Val Ala Thr Ser His Tyr Arg Asn Ala Asp Ala Phe Ile Ser
 410 415 420
 att cat tat gat agc ttt cca aat gcg tcc gtc agg gga aat acg gcc 1829
 Ile His Tyr Asp Ser Phe Pro Asn Ala Ser Val Arg Gly Asn Thr Ala
 425 430 435 440
 tat tac tac agc ccg tcc aaa gac cgg aag ctc gca gca gac gtg cag 1877
 Tyr Tyr Tyr Ser Pro Ser Lys Asp Arg Lys Leu Ala Ala Asp Val Gln
 445 450 455
 tcc gag atc gaa agg cac tcg cct ctg cca agc cgc ggc gta cta ttc 1925
 Ser Glu Ile Glu Arg His Ser Pro Leu Pro Ser Arg Gly Val Leu Phe
 460 465 470
 ggg gac tac ttc gta tta aga gaa aat aaa cag ccc gcc gca ttg ttt 1973
 Gly Asp Tyr Phe Val Leu Arg Glu Asn Lys Gln Pro Ala Ala Leu Phe
 475 480 485
 gaa ctc ggc tac ttg agc cat cct caa gaa gaa gcg gta gtc agc acg 2021
 Glu Leu Gly Tyr Leu Ser His Pro Gln Glu Glu Ala Val Val Ser Thr
 490 495 500
 aac gct tac aga gaa aga gtg aca gac ggc atc aga agc ggt cta gaa 2069
 Asn Ala Tyr Arg Glu Arg Val Thr Asp Gly Ile Arg Ser Gly Leu Glu
 505 510 515 520
 aac tat ttt gac taatttaaaa agctcccaat cgggagcttt ttatgctttc 2121
 Asn Tyr Phe Asp
 gaatccataa taaacgtgac gggacccgaa tttgtcagct tgacatccat catttctcca 2181
 aatcttcccg tttcgacagt gacgcctttt gcgcgaagca tgctgttcca ctcttcgtac 2241
 aattgaagcg cctgatcggg ctttgccgct tttgtaaaat tcggccgtct tccttttttc 2301
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 gacaggttca tcttttcgcc ttcattctca aaaattcgca gattgacaag cttctccgcc 2421
 aaatatgcgg catcctcgct cgtatcttcg tgcgtcacgc cgacaagcac catcaagccg 2481
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<210> 102

<211> 524

<212> PRT

<213> Bacillus licheniformis

<400> 102

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 20 25 30

Glu Ala Val Ile Ala Thr Asp Glu Ile Asn Val Arg Ser Gly Pro Gly
 35 40 45

Leu Ser His Glu Ile Val Ser Val Val Ser Arg Asn Glu Ser Tyr Pro
 50 55 60

Ile Leu Glu Glu Arg Gly Asp Trp Val Gln Ile Gln Leu Asn Gly Gly
 65 70 75 80

Gln Lys Gly Trp Val Val Ser Trp Leu Ile Lys Lys Lys Ser Gln Val
 85 90 95

Ser Ser Gly Ser Asp Ser Ala Ser Gly Lys Val Thr Ser Ser Glu Ala
 100 105 110

Asn Leu Arg Ile Arg Lys Gly Pro Gly Thr Ser Tyr Glu Val Gln Gly
 115 120 125

Val Phe Pro Glu Gly Glu Gln Ala Asp Leu Leu Lys Thr Asp Gly Lys
 130 135 140

Trp Ile Lys Ile Ser Tyr Gln Asn Ile Thr Gly Trp Val Tyr Ser Asp
 145 150 155 160

Tyr Val Asn Gln Gly Ser Gly Ala Lys Gln Ser Gln Ser Ser Ser Ser
 165 170 175

His Ala Ser Ser Ser Lys Ser Gly Thr Val Gly Val Ser Thr Leu Asn
 180 185 190

Val Arg Ser Thr Ala Ser His Gln Gly Arg Ile Ile Ala Thr Leu Gln
 195 200 205

Arg Asn Ala Ser Val Thr Ile Leu Asn Glu Gln His Gly Trp Tyr Glu
 210 215 220

Ile Glu Phe Asn Gly Gln Lys Gly Trp Ala Ala Ser His Tyr Ile Leu
 225 230 235 240

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Glu Gly Asn Lys Gln Asn Ser Gly Thr Ser Gly Thr Ser Ser Ser Ser
245 250 255

Glu Ala Lys Arg Gln Gly Thr Ile Val Tyr Glu Ser Thr Asn Val Arg
260 265 270

Ser Gly Ala Ser Thr Ser Ser Ala Ile Val Lys Arg Thr Gly Lys Gly
275 280 285

Glu Ser Tyr Pro Ile Val Ser Thr Lys Gly Asp Trp Tyr Glu Ile Lys
290 295 300

Leu Ser Asn Gly Asp Ser Ala Tyr Val Ala Ser Trp Val Val Gln Thr
305 310 315 320

Val Asp Gln Ala Gly Ser Ala Gly Asp Ser Lys Ser Ala Ala Pro Pro
325 330 335

Leu Ala Lys Arg Ser Ser Ser Gly Gly Thr Ile Lys Asn Lys Thr Val
340 345 350

Val Ile Asp Ala Gly His Gly Gly His Asp Ser Gly Thr Ile Gly Thr
355 360 365

Arg Gly Thr Leu Glu Lys Arg Leu Thr Ile Lys Thr Ala Thr Leu Leu
370 375 380

Ala Ala Lys Leu Arg Ala Asp Gly Val Asn Val Tyr Met Thr Arg Asn
385 390 395 400

Asp Asp Ser Phe Val Ser Leu Gln Ser Arg Val Ala Thr Ser His Tyr
405 410 415

Arg Asn Ala Asp Ala Phe Ile Ser Ile His Tyr Asp Ser Phe Pro Asn
420 425 430

Ala Ser Val Arg Gly Asn Thr Ala Tyr Tyr Tyr Ser Pro Ser Lys Asp
435 440 445

Arg Lys Leu Ala Ala Asp Val Gln Ser Glu Ile Glu Arg His Ser Pro
450 455 460

Leu Pro Ser Arg Gly Val Leu Phe Gly Asp Tyr Phe Val Leu Arg Glu
465 470 475 480

Asn Lys Gln Pro Ala Ala Leu Phe Glu Leu Gly Tyr Leu Ser His Pro
485 490 495

Gln Glu Glu Ala Val Val Ser Thr Asn Ala Tyr Arg Glu Arg Val Thr
500 505 510

<213> Bacillus licheniformis

<223>

[illegible]

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tca ttt acg gca tac gag ctg atc agc caa gac ggc gaa ccg ctt cat Ser Phe Thr Ala Tyr Glu Leu Ile Ser Gln Asp Gly Glu Pro Leu His 120 125 130	917
aaa acc att cat gca ccc gta agc ctt aca tat gat gat gta tta aaa Lys Thr Ile His Ala Pro Val Ser Leu Thr Tyr Asp Asp Val Leu Lys 135 140 145	965
aat acg atc atc ggc tgc ttg acg gtg atg att gac aga gaa caa acg Asn Thr Ile Ile Gly Cys Leu Thr Val Met Ile Asp Arg Glu Gln Thr 155 160 165	1013
ggt gat atc cgg atg ccg aat att aga acc cgc cag gat ttg gcg aca Gly Asp Ile Arg Met Pro Asn Ile Arg Thr Arg Gln Asp Leu Ala Thr 170 175 180	1061
tgg ctg tcc gta tta aag cgg ggg ttc aag gca tat gga ctg aac gaa Trp Leu Ser Val Leu Lys Arg Gly Phe Lys Ala Tyr Gly Leu Asn Glu 185 190 195	1109
ccc ctc gcg gaa tac cgc atc gtt gaa aca tcg atc tcc aga aac aag Pro Leu Ala Glu Tyr Arg Ile Val Glu Thr Ser Ile Ser Arg Asn Lys 200 205 210	1157
tgg aag gcg gcg cga aaa acc tgg tac gta tac agg gaa atc gaa cga Trp Lys Ala Ala Arg Lys Thr Trp Tyr Val Tyr Arg Glu Ile Glu Arg 215 220 225 230	1205
ctt cac ttg atg aaa gcg aca tgg tgc ttt ttc cat tac gct aag aac Leu His Leu Met Lys Ala Thr Trp Cys Phe Phe His Tyr Ala Lys Asn 235 240 245	1253
gca gta atg aaa aga tta taacggcatt gacagaaaag gtgattgaaa Ala Val Met Lys Arg Leu 250	1301
gtgaaagcag atcaattcat acacgtcata gtagcgacag gtgaatgggg gcaggatcag	1361
ctaagataca gaaggcaccg ccttgctgag tttttagcag gccgcaagga gacgaaggaa	1421
gtcatttggg tttgtccgtc tgaaaatcct tcccgtgaga cttttacatt gcttgacaac	1481
ggaatcaagc aatttgcagt caaagatttt ttgaaaaaga aaatattcag gtttgcccgc	1541
tacaaagatg ttttctatca aagcaagctg aagccgctgc ttgaccggct gaaagaagac	1601
gttcagggag aaaaggtgtg cttatggtac accttccccg gctttccgct gctgtcgtcg	1661
ctttatcaat gggatcaggt catctatgac tgcagcgacc tgtgggcggc cccgatcagc	1721
ggtagccaaa gccttgtctc aggattcagg caaaaggtca tttttgaagc tga	1774

<210> 104

<211> 252

<212> PRT

<213> Bacillus licheniformis

<400> 104

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 Ala Glu Glu Phe Ile Glu Lys Thr Ile Lys Ser Val Leu Asn Gln Thr
 20 25 30
 Phe Ser Asp Trp Glu Met Ile Ile Ala Asp Asp Cys Ser Thr Asp Gly
 35 40 45
 Thr Arg Asp Ile Leu Lys Arg Tyr Glu Glu Asp Asp Glu Arg Ile His
 50 55 60
 Ala Ile Phe Leu Lys Glu Asn Gln Gly Ala Ala Ala Arg Asn Ala
 65 70 75 80
 Ala Leu Ser Lys Ala Glu Gly Arg Tyr Val Ala Phe Leu Asp Ser Asp
 85 90 95
 Asp Val Trp Lys Ala Glu Lys Leu Asp Lys Gln Leu Ala Phe Met Arg
 100 105 110
 Lys His Gln His Ala Phe Ser Phe Thr Ala Tyr Glu Leu Ile Ser Gln
 115 120 125
 Asp Gly Glu Pro Leu His Lys Thr Ile His Ala Pro Val Ser Leu Thr
 130 135 140
 Tyr Asp Asp Val Leu Lys Asn Thr Ile Ile Gly Cys Leu Thr Val Met
 145 150 155 160
 Ile Asp Arg Glu Gln Thr Gly Asp Ile Arg Met Pro Asn Ile Arg Thr
 165 170 175
 Arg Gln Asp Leu Ala Thr Trp Leu Ser Val Leu Lys Arg Gly Phe Lys
 180 185 190
 Ala Tyr Gly Leu Asn Glu Pro Leu Ala Glu Tyr Arg Ile Val Glu Thr
 195 200 205
 Ser Ile Ser Arg Asn Lys Trp Lys Ala Ala Arg Lys Thr Trp Tyr Val
 210 215 220
 Tyr Arg Glu Ile Glu Arg Leu His Leu Met Lys Ala Thr Trp Cys Phe
 225 230 235 240
 Phe His Tyr Ala Lys Asn Ala Val Met Lys Arg Leu
 245 250

<210> 105

<211> 1309

<212> DNA

<213> *Bacillus licheniformis*

<220>

<221> CDS

<222> (485)..(808)

<223>

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<400> 105
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aatcaacacc gaaaatgaag gaactcccgg tcagatgaaa aaaatcgtcg acacagtgaa      180
gaaaaaggac gtcccggcct tattcgtgga gacaagcggt gacccgcgga gcatggaaaag      240
cctttcagcc gaaacgggcg tgccgattaa agcaaaagtc ttcaccgatt cgatcgaaaa      300
gcccggtgga agcgggagat tcctattata agatgatgaa agaaaacctt gaccggatcc      360
atcaaggcct cgccgaataa ccaatgaact gctgtacagg atgtacagca gtttttttct      420
tatgtttttc cgattttaaa gcagggtaca acgaagggaa aacgaggaaa aaggagtgtg      480
tttc gtg aaa tct gga tat gag gaa tgc atc aaa gcc tgc cga gaa tgt      529
    Val Lys Ser Gly Tyr Glu Glu Cys Ile Lys Ala Cys Arg Glu Cys
      1          5          10          15

ctt gaa gcc tgc aac cac tgc ttt gac aaa tgt ctg atg gaa gaa gag      577
Leu Glu Ala Cys Asn His Cys Phe Asp Lys Cys Leu Met Glu Glu Glu
      20          25          30

gct ggg atg atg gcc gaa tgc atc cgt ctt gac cgg gaa tgc gcg gag      625
Ala Gly Met Met Ala Glu Cys Ile Arg Leu Asp Arg Glu Cys Ala Glu
      35          40          45

atg tgc ggt tac gca att caa gcc atg acg cgc aac agc ccg tat gcc      673
Met Cys Gly Tyr Ala Ile Gln Ala Met Thr Arg Asn Ser Pro Tyr Ala
      50          55          60

gaa gat att tgc cag ctt tgc gca aag gtt tgc gaa gct tgc ggc aat      721
Glu Asp Ile Cys Gln Leu Cys Ala Lys Val Cys Glu Ala Cys Gly Asn
      65          70          75

gaa tgc agc cag cac aag cat gac cac tgc caa ttt tgc gct gaa agc      769
Glu Cys Ser Gln His Lys His Asp His Cys Gln Phe Cys Ala Glu Ser
      80          85          90          95

tgc ttt gca tgc gcg gaa gcg tgc aga aaa atg gct tct taacttgaaa      818
Cys Phe Ala Cys Ala Glu Ala Cys Arg Lys Met Ala Ser
      100          105

catccggccc tcgagccgga ttttttatg taggaaatgt ttattttttc tccttcccc      878
tttctaaact gatacaatat gactataaaa gggggtttta tcatgaaaga cagcgtgttt      938
caaatgactt ctgacacata tcaatctctc agcgattcag aacggcattt gctcgagtac      998

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atttatcagc acttagacgt catcgccact ttatcgattg taaaattaag cgaggatgca 1058
 aatgtttcaa cagccacgat tgtcagggtta atgaaaaaac tcggatatga cggctacact 1118
 tcttttaagt atgcattaaa agaaaaacac cacctcggac acgctccgct gatggatgat 1178
 atcgacagcc aaattaaaca ggccgtgcta aagaatgaaa gagaagttct ggatacgatt 1238
 aagatgcttg atatcggggt gatcgaagat gccattcaaa aaatcagcaa tgccgaaaaa 1298
 gtttacatct t 1309

<210> 106

<211> 108

<212> PRT

<213> Bacillus licheniformis

<400> 106

Val Lys Ser Gly Tyr Glu Glu Cys Ile Lys Ala Cys Arg Glu Cys Leu
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 20 25 30

Gly Met Met Ala Glu Cys Ile Arg Leu Asp Arg Glu Cys Ala Glu Met
 35 40 45

Cys Gly Tyr Ala Ile Gln Ala Met Thr Arg Asn Ser Pro Tyr Ala Glu
 50 55 60

Asp Ile Cys Gln Leu Cys Ala Lys Val Cys Glu Ala Cys Gly Asn Glu
 65 70 75 80

Cys Ser Gln His Lys His Asp His Cys Gln Phe Cys Ala Glu Ser Cys
 85 90 95

Phe Ala Cys Ala Glu Ala Cys Arg Lys Met Ala Ser
 100 105

<210> 107

<211> 1561

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<223>

<400> 107

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tccaaacagg	aagtcaaagt	ccgcgaagtt	atgattgaag	gcaccccttc	gatcttggaa		180										
ggccaggctc	caaaagtcac	tgaacaaaag	cttttgatgt	acgtttctcc	aagcgaacgc		240										
tccagcatcg	tcacccaga	tggagacaaa	ggggacagca	gca	atg	gct	aga	aaa		295							
				Met	Ala	Arg	Lys										
				1													
aag	aag	cac	aaa	aaa	gac	cat	gaa	gaa	cac	gtg	gat	gag	tct	tgg	ctc		343
Lys	Lys	His	Lys	Lys	Asp	His	Glu	Glu	His	Val	Asp	Glu	Ser	Trp	Leu		
5					10					15					20		
atc	cca	tat	gca	gac	ttg	ctg	aca	ctg	ctt	ttg	gcc	ctg	ttc	atc	gta		391
Ile	Pro	Tyr	Ala	Asp	Leu	Leu	Thr	Leu	Leu	Leu	Ala	Leu	Phe	Ile	Val		
				25					30					35			
ctg	ttt	gcc	atg	agc	tcg	atc	gac	gcc	aag	aag	ttc	gat	atg	ctg	tca		439
Leu	Phe	Ala	Met	Ser	Ser	Ile	Asp	Ala	Lys	Lys	Phe	Asp	Met	Leu	Ser		
			40					45					50				
aaa	tca	ttt	aat	gcc	gta	ttt	acc	ggc	gga	aca	gga	atg	atg	gat	tat		487
Lys	Ser	Phe	Asn	Ala	Val	Phe	Thr	Gly	Gly	Thr	Gly	Met	Met	Asp	Tyr		
		55					60					65					
tcc	agc	ttc	acc	gag	ccg	aaa	acg	agc	aca	acc	gaa	gat	gga	aaa	agc		535
Ser	Ser	Phe	Thr	Glu	Pro	Lys	Thr	Ser	Thr	Thr	Glu	Asp	Gly	Lys	Ser		
	70					75					80						
cct	gac	cag	gca	aaa	gat	ctc	tcc	gaa	gct	caa	aaa	gaa	aaa	gac	aag		583
Pro	Asp	Gln	Ala	Lys	Asp	Leu	Ser	Glu	Ala	Gln	Lys	Glu	Lys	Asp	Lys		
85					90					95					100		
cag	tcg	ctg	aaa	aaa	att	cag	gag	cag	gtc	aac	cgg	ttt	att	aaa	gag		631
Gln	Ser	Leu	Lys	Lys	Ile	Gln	Glu	Gln	Val	Asn	Arg	Phe	Ile	Lys	Glu		
				105					110					115			
aag	aat	ctt	caa	aaa	cag	gtc	aat	acg	aag	ctg	aca	gac	gag	ggc	ctc		679
Lys	Asn	Leu	Gln	Lys	Gln	Val	Asn	Thr	Lys	Leu	Thr	Asp	Glu	Gly	Leu		
			120					125					130				
ctc	ctt	tcc	atc	gag	gat	aat	atc	ttt	ttc	gat	tcc	gga	aaa	gcg	gag		727
Leu	Leu	Ser	Ile	Glu	Asp	Asn	Ile	Phe	Phe	Asp	Ser	Gly	Lys	Ala	Glu		
		135					140					145					
atc	cgc	cag	cag	gac	att	ccg	ctg	gcc	aag	gaa	gta	tcc	gac	ctt	ctc		775
Ile	Arg	Gln	Gln	Asp	Ile	Pro	Leu	Ala	Lys	Glu	Val	Ser	Asp	Leu	Leu		
	150					155					160						
gta	ttg	aac	ccg	ccc	cgc	aat	atc	gta	atc	agc	ggg	cat	acg	gac	aat		823
Val	Leu	Asn	Pro	Pro	Arg	Asn	Ile	Val	Ile	Ser	Gly	His	Thr	Asp	Asn		
165					170					175					18		

10294.000.ST25.txt

Met Arg Ala Val Asn Phe Met Gly Leu Leu Ile Glu Asn Pro Lys Leu
 200 205 210

gac gcc aag atc ttc agc gcg aaa ggc tac ggg gaa ttt aaa ccg atc 967
 Asp Ala Lys Ile Phe Ser Ala Lys Gly Tyr Gly Glu Phe Lys Pro Ile
 215 220 225

gct tca aat gac acc gaa gaa gga aga aga aaa aac aga cgc gtt gaa 1015
 Ala Ser Asn Asp Thr Glu Glu Gly Arg Arg Lys Asn Arg Arg Val Glu
 230 235 240

atc ctt atc ctg ccg atc ggc cag gaa aat ctg aat aaa aaa gaa 1060
 Ile Leu Ile Leu Pro Ile Gly Gln Glu Asn Leu Asn Lys Lys Glu
 245 250 255

taaggaagct gtcttttggc agcttcctta ctctttgccc ttataaatat ttcttgcat 1120
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<213> Bacillus licheniformis

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Asp Met Leu Ser Lys Ser Phe Asn Ala Val Phe Thr Gly Gly Thr Gly
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145 150 155 160
Ser Asp Leu Leu Val Leu Asn Pro Pro Arg Asn Ile Val Ile Ser Gly
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His Thr Asp Asn Val Pro Ile Arg Asn Ser Gln Phe Lys Ser Asn Trp
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His Leu Ser Val Met Arg Ala Val Asn Phe Met Gly Leu Leu Ile Glu
195 200 205
Asn Pro Lys Leu Asp Ala Lys Ile Phe Ser Ala Lys Gly Tyr Gly Glu
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 35 40 45
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 Glu Val Asp Gln Glu Arg Leu Leu Glu Ile Phe Lys Thr Tyr Gly Val
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 195 200 205

Arg Phe Gly Leu Cys Glu Ile Gly Gly Thr Gly Thr Val Phe Lys Ala
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caa Gln 155	gtc Val	aga Arg	aac Asn	cac His	aaa Lys	tat Tyr 160	ccc Pro	gtc Val	atg Met	aaa Lys	atg Met 165	gaa Glu	tat Tyr	tac Tyr	aaa Lys	1013
gac Asp 170	gga Gly	aag Lys	tgg Trp	atc Ile	aac Asn 175	atg Met	gag Glu	aaa Lys	acg Thr	gat Asp 180	tac Tyr	aac Asn	cat His	ttc Phe	gtc Val 185	1061
agc Ser	acc Thr	aat Asn	ctc Leu	ggg Gly 190	aca Thr	agt Ser	ccg Pro	ctt Leu	aaa Lys 195	gtc Val	agg Arg	atc Ile	aca Thr	gat Asp 200	atc Ile	1109
cga Arg	gga Gly	aaa Lys	gtc Val 205	gtc Val	aaa Lys	gac Asp	acg Thr	ata Ile 210	aaa Lys	aag Lys	ctt Leu	ccg Pro	gaa Glu 215	aac Asn	ggg Gly	1157
acg Thr 220	tca Ser	agc Ser	gca Ala	tat Tyr	acc Thr	gta Val	ccg Pro 225	gga Gly	aaa Lys	gta Val	cag Gln 230	ttc Phe	cct Pro	gac Asp		1202
tgatcgatcc	ggaaagaatg	agacggcggc	caaaggcgaa	aagattcgca	ggctttggcc											1262
gccgcttcat	attgacatcc	ggcatttaga	cgccagcaac	aattggctta	ttgatcaata											1322
gcccggtcct	gctcctctgt	atggagctgc	gcccgggaaca	cctccgtacg	gaaaagcccc											1382
aggagctgcc	ccgtagccgt	aataaggcgc	gccgccgtaa	ggtccccgggt	atggcggcgg											1442
gtaagcgtaa	ggtcttgggt	agttaaaaat	cgcgcttccg	agaaatccgc	ccagcaatcc											1502
gccgacaagc	ggcgctccaa	aaccccagaa	taacgggaat	ctggccgggt	atccggcagg											1562
acctgatctc	gaataaagca	tatgagggtt	cattggcttt	tatcctcctt	tatgtctgcc											1622

tatagtaaag gtattcataa agtcgggaaa cgtttgggct attcttcata aatcattttt 1682
 tttgtcattc cgccgtccac cgt 1705

<210> 116

<211> 232

<212> PRT

<213> Bacillus licheniformis

<400> 116

Met Lys Lys Lys Ile Ser Ile Leu Ile Thr Ala Met Phe Leu Thr Ile
 1 5 10 15

Leu Cys Phe Ser Pro Gln Ala Ser Ala Ala Tyr Asn Ser Leu His Thr
 20 25 30

Gly Tyr Ala Thr Tyr Thr Gly Ser Gly Tyr Ser Gly Gly Ala Leu Leu
 35 40 45

Leu Asp Pro Ile Pro Ser Asn Met Lys Ile Thr Ala Leu Asn Pro Thr
 50 55 60

Asp Met Asn Tyr Arg Gly Val Lys Ala Ala Leu Ala Gly Ala Tyr Leu
 65 70 75 80

Arg Val Glu Gly Pro Lys Gly Lys Thr Thr Val Tyr Val Thr Asp Leu
 85 90 95

Tyr Pro Glu Gly Ala Pro Gly Ala Leu Asp Leu Ser Pro Asn Ala Phe
 100 105 110

Arg Glu Ile Gly Asp Met Lys Asp Gly Lys Ile Asp Ile Lys Trp Arg
 115 120 125

Ile Val Lys Ala Pro Ile Thr Gly Asn Phe Thr Tyr Arg Ile Lys Glu
 130 135 140

Gly Ser Ser Gln Trp Trp Ala Ala Ile Gln Val Arg Asn His Lys Tyr
 145 150 155 160

Pro Val Met Lys Met Glu Tyr Tyr Lys Asp Gly Lys Trp Ile Asn Met
 165 170 175

Glu Lys Thr Asp Tyr Asn His Phe Val Ser Thr Asn Leu Gly Thr Ser
 180 185 190

Pro Leu Lys Val Arg Ile Thr Asp Ile Arg Gly Lys Val Val Lys Asp
 195 200 205

10294.000.ST25.txt

Thr Ile Lys Lys Leu Pro Glu Asn Gly Thr Ser Ser Ala Tyr Thr Val
 210 215 220

Pro Gly Lys Val Gln Phe Pro Asp
 225 230

<210> 117

<211> 1687

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1184)

<223>

<400> 117
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 tacggtgcgc attatatggc gaaagacggc aagaaagcat aagacatcgt caagtattat 120
 tacaaaggaa cagccgtatc caatgcagat gaatttttaa ataaatacat ggcgaaaaaa 180
 taaaacaaaa gacgtctgcc tcttggcggc gtctttttga atatcatcga aatttggcat 240
 tcccatgaat ttgatgcacg ctaaattatt atacaaatat ttctaaaaac atgtgccgga 300
 gggcttgctg aacagcgta aaaggccgca aacgccgtat caacaatagg gggtcacagg 360
 tataaagtct attttatata cttgttgtat gatgaattga ataacgagga aaaggagaca 420
 tgccctatatt atttctccct ggtgttcttc tacgataata atgtgttaac gactttattt 480
 cagaaagggg aaaggggagaa atg aag aag aag atg aca ttg ggc att ttg acc 533
 Met Lys Lys Lys Met Thr Leu Gly Ile Leu Thr 10
 1 5
 gct atg gtt ctc agt ctt ggt tcg cct gct ttt gca gct gag aaa aaa 581
 Ala Met Val Leu Ser Leu Gly Ser Pro Ala Phe Ala Ala Glu Lys Lys 25
 15 20
 cag gag gta aca gtt gcc gaa gat gcg ccc aac gtt gcg att atg ctt 629
 Gln Glu Val Thr Val Ala Glu Asp Ala Pro Asn Val Ala Ile Met Leu 40
 30 35
 gat gca agc ggc agc atg gct aaa aag atc ggc ggg gtc tca aaa tac 677
 Asp Ala Ser Gly Ser Met Ala Lys Lys Ile Gly Gly Val Ser Lys Tyr 55
 45 50
 gag ctt gcc aaa aat gaa gcg ttc agc ttt ggt tcc aag ctt gaa aat 725
 Glu Leu Ala Lys Asn Glu Ala Phe Ser Phe Gly Ser Lys Leu Glu Asn 75
 60 65 70
 gca aac gtg ctc atg aga gtt ttc ggt tca gag gga aac aat aaa aat 773

10294.000.ST25.txt

Ala Asn Val Leu Met Arg Val Phe Gly Ser Glu Gly Asn Asn Lys Asn
80 85 90

tcc gga aaa gtg cag tcc tgc aat gca atc aga ggg gtg tac ggc ttc 821
Ser Gly Lys Val Gln Ser Cys Asn Ala Ile Arg Gly Val Tyr Gly Phe
95 100 105

caa acg tat gac gag caa agc ttc cgc aat tcc tta aac ggc atc gga 869
Gln Thr Tyr Asp Glu Gln Ser Phe Arg Asn Ser Leu Asn Gly Ile Gly
110 115 120

ccg acc gga tgg aca ccg atc gca aac gcg ctg caa gat gca aaa aac 917
Pro Thr Gly Trp Thr Pro Ile Ala Asn Ala Leu Gln Asp Ala Lys Asn
125 130 135

gcg ctt gac cag ctg gac aac aac ggg aaa aac gtc gtc tat ctg ctg 965
Ala Leu Asp Gln Leu Asp Asn Asn Gly Lys Asn Val Val Tyr Leu Leu
140 145 150 155

aca gac ggt gag gaa aca tgc gga ggc aat ccg gta aaa gtc gca aca 1013
Thr Asp Gly Glu Glu Thr Cys Gly Gly Asn Pro Val Lys Val Ala Thr
160 165 170

gaa ctg cgc aaa tcc aat gcg gtt gtc aac gtg atc ggc ttt gat tat 1061
Glu Leu Arg Lys Ser Asn Ala Val Val Asn Val Ile Gly Phe Asp Tyr
175 180 185

gaa gga gac ttc cac gga caa ttg acc agt atc gca gca gct ggc ggc 1109
Glu Gly Asp Phe His Gly Gln Leu Thr Ser Ile Ala Ala Ala Gly Gly
190 195 200

ggt gaa tat ttc cag gca aaa act aaa aat gac atc aaa aga att ttt 1157
Gly Glu Tyr Phe Gln Ala Lys Thr Lys Asn Asp Ile Lys Arg Ile Phe
205 210 215

act cag gaa gca att gag ctt tct aaa taaactggaa aaaagctgtg 1204
Thr Gln Glu Ala Ile Glu Leu Ser Lys
220 225

gacatgtttc cgcagctttc cttttgtgat gaaaagattg tcaaaagtca agaaaaatac 1264

tttacaaata ttaagttatt gtgtcagagc gttgaacctt gctgcgtcct ttggaggggt 1324

tatttgtcgt aacggtagct ttattgggat gaaatcggcc ttttagcaga cttttttgat 1384

aggtcttaag tgaatgcgtc gatcgattat cgtaaggatt atgaagaatt tgtgaatttg 1444

aaaaggagat ccggcctatt tatttctatc aagccttctt ttacgatgtt ggtggacttg 1504

atctcatgcg gaagatcggg ccgaaaaaac aaatgcggaa aggaaagtga gaaagttgaa 1564

aaagagggtt gctctgttga caacgttcac catgcttttg tcattggcgc cggcagcagc 1624

ttttgcggct gaaaacggaa atgcggacaa cagcaaaaaa gatgtcaatg ttgcagttgt 1684

gct 1687

<210> 118

<211> 228

<212> PRT

<213> Bacillus licheniformis

<400> 118

Met Lys Lys Lys Met Thr Leu Gly Ile Leu Thr Ala Met Val Leu Ser
 1 5 10 15
 Leu Gly Ser Pro Ala Phe Ala Ala Glu Lys Lys Gln Glu Val Thr Val
 20 25 30
 Ala Glu Asp Ala Pro Asn Val Ala Ile Met Leu Asp Ala Ser Gly Ser
 35 40 45
 Met Ala Lys Lys Ile Gly Gly Val Ser Lys Tyr Glu Leu Ala Lys Asn
 50 55 60
 Glu Ala Phe Ser Phe Gly Ser Lys Leu Glu Asn Ala Asn Val Leu Met
 65 70 75 80
 Arg Val Phe Gly Ser Glu Gly Asn Asn Lys Asn Ser Gly Lys Val Gln
 85 90 95
 Ser Cys Asn Ala Ile Arg Gly Val Tyr Gly Phe Gln Thr Tyr Asp Glu
 100 105 110
 Gln Ser Phe Arg Asn Ser Leu Asn Gly Ile Gly Pro Thr Gly Trp Thr
 115 120 125
 Pro Ile Ala Asn Ala Leu Gln Asp Ala Lys Asn Ala Leu Asp Gln Leu
 130 135 140
 Asp Asn Asn Gly Lys Asn Val Val Tyr Leu Leu Thr Asp Gly Glu Glu
 145 150 155 160
 Thr Cys Gly Gly Asn Pro Val Lys Val Ala Thr Glu Leu Arg Lys Ser
 165 170 175
 Asn Ala Val Val Asn Val Ile Gly Phe Asp Tyr Glu Gly Asp Phe His
 180 185 190
 Gly Gln Leu Thr Ser Ile Ala Ala Ala Gly Gly Gly Glu Tyr Phe Gln
 195 200 205
 Ala Lys Thr Lys Asn Asp Ile Lys Arg Ile Phe Thr Gln Glu Ala Ile
 210 215 220
 Glu Leu Ser Lys
 225

<210> 119

<211> 1428

<212> DNA

<213> Bacillus licheniformis .10294.000.ST25.txt

<220>

<221> CDS

<222> (501)..(944)

<223>

<400> 119
attcacgcaa gggttcctatt tgaaacccgc ttctacgatg aacgaaaaaa cggcgtcgta 60
tccgccggaa ggctgaacga actgatggaa gaagctcaga aagaagcgtt ttgcggtgcg 120
cttggcgagt atcatccgta tttttgggca tcaaagcttc atttttatat tacgtctggt 180
ccgttttaca attttcctta tacgttcggc tacttgtttt cgcttggcat ttacgcgcaa 240
gcgctgaaag aggggtgcggc atttgaagaa aaatatattg ctctcttaaa agatacagcc 300
tccatgtctg ttgaagaact ggccatgaag catctcggcg cccgatctgac gaagcgggat 360
ttctgggaag cggccattca gccggctgtc cgagatgcag aagcattttt agcgatgaca 420
taaagtcttc cgcttagatt gaatgagttt ccgcaaagtg gacatagcta aggataatgt 480
gcatagagga gatgaacggg atg aat caa ttt cgg atg gcc gtt atc gct ctc 533
Met Asn Gln Phe Arg Met Ala Val Ile Ala Leu
1 5 10
gtc ctg atc ctg atg acc ggc tgc ggc tcc ata gcg gaa gaa cat gcg 581
Val Leu Ile Leu Met Thr Gly Cys Gly Ser Ile Ala Glu Glu His Ala
15 20 25
gaa ggc aag gag gcc gtt ccc gat aac gcc cct gtt tca gat gtg aaa 629
Glu Gly Lys Glu Ala Val Pro Asp Asn Ala Pro Val Ser Asp Val Lys
30 35 40
agc gtg cct tac gct gca ttt gca ttg gaa gtg aac tat ggc cat gga 677
Ser Val Pro Tyr Ala Ala Phe Ala Leu Glu Val Asn Tyr Gly His Gly
45 50 55
aag cac aat acg ttt gaa gcc gta tac gac aaa cag gag cgg gaa gaa 725
Lys His Asn Thr Phe Glu Ala Val Tyr Asp Lys Gln Glu Arg Glu Glu
60 65 70 75
gca tcg att aaa gac tat ctg aac gga gcg gac cgc gaa ggg gag gaa 773
Ala Ser Ile Lys Asp Tyr Leu Asn Gly Ala Asp Arg Glu Gly Glu Glu
80 85 90
gct tta aac gaa atg aaa atg gtt tta agc gag ctt tcg atc gcc aaa 821
Ala Leu Asn Glu Met Lys Met Val Leu Ser Glu Leu Ser Ile Ala Lys
95 100 105
tcc gat cca gag cag gac gtg atc agc aat gtg ctc gag gcc ttc aat 869
Ser Asp Pro Glu Gln Asp Val Ile Ser Asn Val Leu Glu Ala Phe Asn
110 115 120
ctt gac gaa caa tat gac cgg ttt cag ctg cgg gtg aaa tgg cct gat 917
Leu Asp Glu Gln Tyr Asp Arg Phe Gln Leu Arg Val Lys Trp Pro Asp
125 130 135
ggc acg tcc aga atc tat aac gga aaa taaacaaaag agcatttcca 964

Gly Thr Ser Arg Ile Tyr Asn Gly Lys
140 145

aactggaaat gctctttttt gcttaagatt ttaaaaagta tttttcgatg tcatcaagga 1024
acagatacgc tgctttttacg ccgccggccg tcgtccagat cgcacgctcg acttcatggg 1084
cgtttccggt ttttacagcg ttcaattttt tccacagcgg atcgcttgtc caatcgtttt 1144
gccatgtttc agctttctttt ttgctttcgg caggtttata tgtgaaatag aacaggacat 1204
ctccgtccat atcagggatc gattctttat tttccgtcat aaaaacaaat ttgtcgtctt 1264
gtttctcaaa cagtttttcc tgtttttccg gatacttgaa tccgagctga tccaggataa 1324
ttcccgggaa agaatcttta tagtaaatcc ttgattggcc ggccataaat ctgattaccg 1384
acacccgttt ctttttctgg tcgccgagct tgtcgttaa ttcg 1428

<210> 120

<211> 148

<212> PRT

<213> Bacillus licheniformis

<400> 120

Met Asn Gln Phe Arg Met Ala Val Ile Ala Leu Val Leu Ile Leu Met
1 5 10 15

Thr Gly Cys Gly Ser Ile Ala Glu Glu His Ala Glu Gly Lys Glu Ala
20 25 30

Val Pro Asp Asn Ala Pro Val Ser Asp Val Lys Ser Val Pro Tyr Ala
35 40 45

Ala Phe Ala Leu Glu Val Asn Tyr Gly His Gly Lys His Asn Thr Phe
50 55 60

Glu Ala Val Tyr Asp Lys Gln Glu Arg Glu Glu Ala Ser Ile Lys Asp
65 70 75 80

Tyr Leu Asn Gly Ala Asp Arg Glu Gly Glu Glu Ala Leu Asn Glu Met
85 90 95

Lys Met Val Leu Ser Glu Leu Ser Ile Ala Lys Ser Asp Pro Glu Gln
100 105 110

Asp Val Ile Ser Asn Val Leu Glu Ala Phe Asn Leu Asp Glu Gln Tyr
115 120 125

Asp Arg Phe Gln Leu Arg Val Lys Trp Pro Asp Gly Thr Ser Arg Ile
130 135 140

Tyr Asn Gly Lys
145

<210> 121

<211> 1589

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1109)

<223>

<400> 121
agactcgcac gaggggtgaag ttgggttcaac tattttttaaa aatgtaaatc aatatacctat 60
accaaattta taaagtgaac taggataaac tatgtctctt tagggagggtg aaacatatga 120
gcggagggtta cggacacgga agcgggttttg ctttaattgt tgttctgttc attctcttaa 180
tcatcatcgg cgccagctgg ttcggcgggtg gatatggagg ctactaaaaa gttcgtttta 240
aaagtcagca ataacttatg accttctcct tattttacat gttctcctcc tgcttaccgt 300
tgttgactcc atcatgaaag gctctttttt aaaaaagagc ctttttttaa tgcaatacag 360
ataccgaacc tctcctgctg ctgaatgtta atagaaaatt aatgtttttt tcaaaaagag 420
acatgatttt cattctatta atgctattat ttttccatcc tattaataaa taggaaaatt 480
aagagagggga gtgttggttat atg ttt aaa act aag ttc aag aaa aca att ggg 533
Met Phe Lys Thr Lys Phe Lys Lys Thr Ile Gly
1 5 10
att gga ctc gtt gcc gct gcc tgt ttg att tcc gcg tcg gcg gca agc 581
Ile Gly Leu Val Ala Ala Ala Cys Leu Ile Ser Ala Ser Ala Ala Ser
15 20 25
gct gcg tcg caa aat gaa agc gat gtt aaa gtg aaa ctg gac gat cag 629
Ala Ala Ser Gln Asn Glu Ser Asp Val Lys Val Lys Leu Asp Asp Gln
30 35 40
cag cgg aat caa tat acg gtc aaa tct ttc cac tac tta acc gtt gac 677
Gln Arg Asn Gln Tyr Thr Val Lys Ser Phe His Tyr Leu Thr Val Asp
45 50 55
gga aaa aat gtg gat tcg tcg gct caa gcc aac gcc aaa tcc gtc aga 725
Gly Lys Asn Val Asp Ser Ser Ala Gln Ala Asn Ala Lys Ser Val Arg
60 65 70 75
gat gtc aaa gta acc atg gtt ctg ccc aag cag aat aag aac ggc gat 773
Asp Val Lys Val Thr Met Val Leu Pro Lys Gln Asn Lys Asn Gly Asp
80 85 90
ttg ctt gcg tat gga ttt acg agc aag gtt act tta gaa gcc ttt atc 821
Leu Leu Ala Tyr Gly Phe Thr Ser Lys Val Thr Leu Glu Ala Phe Ile
95 100 105

10294.000.ST25.txt

gcg aaa gac aag cag agg ctt gag aag caa ttc aaa cct tct gcc agc 869
Ala Lys Asp Lys Gln Arg Leu Glu Lys Gln Phe Lys Pro Ser Ala Ser
110 115 120

ggt ccc tgc tgt acc gat ttc tat gaa tat aaa aat aaa ggc ggg cag 917
Gly Pro Cys Cys Thr Asp Phe Tyr Glu Tyr Lys Asn Lys Gly Gly Gln
125 130 135

tat att tac tgg aga gac gga ttt aaa aac ttg cca tcc agc tgg aat 965
Tyr Ile Tyr Trp Arg Asp Gly Phe Lys Asn Leu Pro Ser Ser Trp Asn
140 145 150 155

gac aga att tca tgc tta agt acg gcg tct cct tca tca agc tat tca 1013
Asp Arg Ile Ser Ser Leu Ser Thr Ala Ser Pro Ser Ser Ser Tyr Ser
160 165 170

acg acg ctg tgg gag cat act tca act caa gga tac ggc aaa ggc gtt 1061
Thr Thr Leu Trp Glu His Thr Ser Thr Gln Gly Tyr Gly Lys Gly Val
175 180 185

ttg ttt aga cat tcc gat tgg tac ggc act aat tcg agc tcg gca ccc 1109
Leu Phe Arg His Ser Asp Trp Tyr Gly Thr Asn Ser Ser Ser Ala Pro
190 195 200

tgataaatta cttttttttg cgatgccggt gttgttgatc ggttcatcat gaccgataca 1169

gctgatgaca tggatggtag tcatattccc cgggagccgt ttaacatcag attctgccgc 1229

ctgctttaaa aatgccttga gatctgtatc cgctttttgt tcgttcaggt gcaggagttt 1289

aacatacata tcatagatca gctgttttgt cagttcagac atagtcaatg gacagtcctt 1349

tcttttttatt ttccggttaa caaaatatatt taatagttta tttcaggatt tgtcaatatt 1409

atgataaggt gaaatcagat aacaaatgtg ttttgtttat catgaaacaa caccaaaaag 1469

gagaatcgct gatgaatatt gaaggaatag agatggaagt tcgctgcaca ggcgatgtat 1529

gttcagatgc ccttgaattt ttgagacgcc ataaccacga aaaaacagcc gaacattcga 1589

<210> 122

<211> 203

<212> PRT

<213> Bacillus licheniformis

<400> 122

Met Phe Lys Thr Lys Phe Lys Lys Thr Ile Gly Ile Gly Leu Val Ala
1 5 10 15

Ala Ala Cys Leu Ile Ser Ala Ser Ala Ala Ser Ala Ala Ser Gln Asn
20 25 30

Glu Ser Asp Val Lys Val Lys Leu Asp Asp Gln Gln Arg Asn Gln Tyr
35 40 45

Thr Val Lys Ser Phe His Tyr Leu Thr Val Asp Gly Lys Asn Val Asp
50 55 60

10294.000.ST25.txt

ser ser Ala Gln Ala Asn Ala Lys Ser Val Arg Asp Val Lys Val Thr
65 70 75 80

Met Val Leu Pro Lys Gln Asn Lys Asn Gly Asp Leu Leu Ala Tyr Gly
85 90 95

Phe Thr Ser Lys Val Thr Leu Glu Ala Phe Ile Ala Lys Asp Lys Gln
100 105 110

Arg Leu Glu Lys Gln Phe Lys Pro Ser Ala Ser Gly Pro Cys Cys Thr
115 120 125

Asp Phe Tyr Glu Tyr Lys Asn Lys Gly Gly Gln Tyr Ile Tyr Trp Arg
130 135 140

Asp Gly Phe Lys Asn Leu Pro Ser Ser Trp Asn Asp Arg Ile Ser Ser
145 150 155 160

Leu Ser Thr Ala Ser Pro Ser Ser Ser Tyr Ser Thr Thr Leu Trp Glu
165 170 175

His Thr Ser Thr Gln Gly Tyr Gly Lys Gly Val Leu Phe Arg His Ser
180 185 190

Asp Trp Tyr Gly Thr Asn Ser Ser Ser Ala Pro
195 200

<210> 123

<211> 1522

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1019)

<223>

<400> 123

taaataaaaat aaatgaaagc cgcaatgaaa aacggcagcg tcgttttgga agatccgaga	60
tacaggccta aaagcgggcc gaagacgacg ccgagggtga tcgcggtata gcggagatta	120
aagacgaaaa ggcgcgtttc gggtttggaat acgtctgaaa gcagcgctct tgaagtcggt	180
tcaaacaaag cgcggcataa tccgtttaag gcattcatga taaagaatgt ccagacatga	240
tcggcgagtg caaaaccggc gaacacgaac gtccagccga aaatcgagac gagcatgatg	300

10294.000.ST25.txt

gttttccggc cgaacctgtc tgataagtac ccgccataaa agcttgccgc aattccgatc 360
 agagagctcg ctgcaatgac agctcccgca aagccggaag aggcgccttt cacttggtgc 420
 aaataaattg ctaaaaaagg gatgactcat ggcgtgttcc tcatgcgctt taaggtaagg 480
 caaaaaagaa ggtgatattg atg tac agc cga agc aag ttc aaa atc ggt tta 533
 Met Tyr Ser Arg Ser Lys Phe Lys Ile Gly Leu
 1 5 10
 ttg ctt att gga agt ctg ctg gcc gcg ctc agc ttt cac ctg gag gcc 581
 Leu Leu Ile Gly Ser Leu Leu Ala Ala Leu Ser Phe His Leu Glu Ala
 15 20 25
 ttg gcc gaa aag ccg gct aaa gtt caa atc cag ctt gaa aag gtt tat 629
 Leu Ala Glu Lys Pro Ala Lys Val Gln Ile Gln Leu Glu Lys Val Tyr
 30 35 40
 ctg gac gga gac gtt gga att gag aat aaa gta gag gcc gct cgc aca 677
 Leu Asp Gly Asp Val Gly Ile Glu Asn Lys Val Glu Ala Ala Arg Thr
 45 50 55
 ctg gaa gac ttt aaa gct gct tat aaa ggg tgg cag ctc atc gat cag 725
 Leu Glu Asp Phe Lys Ala Ala Tyr Lys Gly Trp Gln Leu Ile Asp Gln
 60 65 70 75
 aaa aag ggg ttt att ctg ttt cgc aaa cag gtg gac gac att tct ccc 773
 Lys Lys Gly Phe Ile Leu Phe Arg Lys Gln Val Asp Asp Ile Ser Pro
 80 85 90
 ctc agc aaa aca aac ggt tat atc gga gtg act gaa gat ggc gtg att 821
 Leu Ser Lys Thr Asn Gly Tyr Ile Gly Val Thr Glu Asp Gly Val Ile
 95 100 105
 tcg act ttt cac ggt cgc ccg ggc atc tta tca gaa ccc att caa tcg 869
 Ser Thr Phe His Gly Arg Pro Gly Ile Leu Ser Glu Pro Ile Gln Ser
 110 115 120
 ttt ttt cag att gat ata aag cgg ctg gaa agc cgg atg gcg gat gat 917
 Phe Phe Gln Ile Asp Ile Lys Arg Leu Glu Ser Arg Met Ala Asp Asp
 125 130 135
 ctg cgc aaa ggg ata cca tac cgc acg aaa aag gaa ttt gaa cat gtc 965
 Leu Arg Lys Gly Ile Pro Tyr Arg Thr Lys Lys Glu Phe Glu His Val
 140 145 150 155
 att gaa gcc gta aaa tca tcc gga agc caa cat cat gta gaa gat atg 1013
 Ile Glu Ala Val Lys Ser Ser Gly Ser Gln His His Val Glu Asp Met
 160 165 170
 aag aca tgacgctgtt atgtcttttt tcagctgcag acagaagctt ttttagcgaa 1069
 Lys Thr
 catatgttaa ctttttcatt ctgcttttgc ctgttttgtg ttacaatgaa gagcagtcaa 1129
 agaggtgaat gaacgttgat cgaattcgta aaagggacga ttgattatgt atcgcccaa 1189
 tatattgtca ttgaaaacgg cgggatcggc tatcagatct tcacgccaaa tccgtttatt 1249
 tataagaaaa acagcaaaga aacaatctat acataccatt atgtaagaga agacacgaat 1309
 gcgctgtacg gcttttcgac aaggggaagaa aaaatgctgt ttacgaaaat gctgaatgtt 1369
 acgggggatcg gcccaaaagg agcgttgcg atcctcgctt ccggcgatcc gggagcggtg 1429
 attgaagcga tcgagaatga ggacgaagca tttctcgtca aatttcccg cgtaggcaaa 1489

aaaacggcaa ggcagatcat ccttgacctg aaa

1522

<210> 124

<211> 173

<212> PRT

<213> Bacillus licheniformis

<400> 124

Met Tyr Ser Arg Ser Lys Phe Lys Ile Gly Leu Leu Leu Ile Gly Ser
1 5 10 15Leu Leu Ala Ala Leu Ser Phe His Leu Glu Ala Leu Ala Glu Lys Pro
20 25 30Ala Lys Val Gln Ile Gln Leu Glu Lys Val Tyr Leu Asp Gly Asp Val
35 40 45Gly Ile Glu Asn Lys Val Glu Ala Ala Arg Thr Leu Glu Asp Phe Lys
50 55 60Ala Ala Tyr Lys Gly Trp Gln Leu Ile Asp Gln Lys Lys Gly Phe Ile
65 70 75 80Leu Phe Arg Lys Gln Val Asp Asp Ile Ser Pro Leu Ser Lys Thr Asn
85 90 95Gly Tyr Ile Gly Val Thr Glu Asp Gly Val Ile Ser Thr Phe His Gly
100 105 110Arg Pro Gly Ile Leu Ser Glu Pro Ile Gln Ser Phe Phe Gln Ile Asp
115 120 125Ile Lys Arg Leu Glu Ser Arg Met Ala Asp Asp Leu Arg Lys Gly Ile
130 135 140Pro Tyr Arg Thr Lys Lys Glu Phe Glu His Val Ile Glu Ala Val Lys
145 150 155 160Ser Ser Gly Ser Gln His His Val Glu Asp Met Lys Thr
165 170

<210> 125

<211> 1492

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(989)

<223>

<400> 125

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gacgggggac attcttgcga tgaataccgg tatgattttg ctgacggcgc tgcattatgt    360
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aattgaaagc cgctgatgga tcctcttcat agtttttagct tttgcgggga agctaataatt    480
aaaaaagaag gggagttccc atg cga aga atc agt ctc att tac ccg ctc atc    533
                        Met Arg Arg Ile Ser Leu Ile Tyr Pro Leu Ile
                        1          5          10

ctg ctg ttt ttt acc ggg tta ttc gta ttt cag ccg cag gca tct gca      581
Leu Leu Phe Phe Thr Gly Leu Phe Val Phe Gln Pro Gln Ala Ser Ala
                        15          20          25

aaa caa gct tgc ccg gca gtc atg cag atg aac acg gtc gaa ggt cag      629
Lys Gln Ala Ser Pro Ala Val Met Gln Met Asn Thr Val Glu Gly Gln
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cgc gtc gtc att ccc gcc gaa ggc cag aag acg atc gtt cat ttt tgg      677
Arg Val Val Ile Pro Ala Gln Gly Gln Lys Thr Ile Val His Phe Trp
                        45          50          55

acg acc tgg tgc ccg cca tgc cgt gaa gag ctt ccg cga ttc caa tcc      725
Thr Thr Trp Cys Pro Pro Cys Arg Glu Glu Leu Pro Arg Phe Gln Ser
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tac tat gaa agc aag caa tcc ggc gtc aag ctc gtg acc gtt aat tta      773
Tyr Tyr Glu Ser Lys Gln Ser Gly Val Lys Leu Val Thr Val Asn Leu
                        80          85          90

ctg aat gcc gaa aag aac gaa cag aag gta aaa cag ttt att aaa gca      821
Leu Asn Ala Glu Lys Asn Glu Gln Lys Val Lys Gln Phe Ile Lys Ala
                        95          100          105

aac aag ctg aca ttt ccg atc gtt ttt gac aaa aag ggt gag atg atg      869
Asn Lys Leu Thr Phe Pro Ile Val Phe Asp Lys Lys Gly Glu Met Met
                        110          115          120

aaa gca tat aaa gtc atg aca att cct acg act ttt ttc ttt aat gaa      917
Lys Ala Tyr Lys Val Met Thr Ile Pro Thr Thr Phe Phe Phe Asn Glu
                        125          130          135

aaa gga gag ctg gag aaa acg ttt gtc ggc ccc att act gta gaa cag      965
Lys Gly Glu Leu Glu Lys Thr Phe Val Gly Pro Ile Thr Val Glu Gln
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160

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tatataaata aaataacttaa tgtttatgct gccgatgagg cggcaatttg ttttttaaga 1199
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gcaatgaaac attgtccgtt gttctgttta ttttagcttt ttgtatcggc ggcttttgcta 1439
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<210> 126

<211> 163

<212> PRT

<213> Bacillus licheniformis

<400> 126

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Ala Val Met Gln Met Asn Thr Val Glu Gly Gln Arg Val Val Ile Pro
35 40 45

Ala Glu Gly Gln Lys Thr Ile Val His Phe Trp Thr Thr Trp Cys Pro
50 55 60

Pro Cys Arg Glu Glu Leu Pro Arg Phe Gln Ser Tyr Tyr Glu Ser Lys
65 70 75 80

Gln Ser Gly Val Lys Leu Val Thr Val Asn Leu Leu Asn Ala Glu Lys
85 90 95

Asn Glu Gln Lys Val Lys Gln Phe Ile Lys Ala Asn Lys Leu Thr Phe
100 105 110

Pro Ile Val Phe Asp Lys Lys Gly Glu Met Met Lys Ala Tyr Lys Val
115 120 125

Met Thr Ile Pro Thr Thr Phe Phe Phe Asn Glu Lys Gly Glu Leu Glu
130 135 140

Gly Lys Ser

<213> Bacillus licheniformis

<223>

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10294.000.ST25.txt

Asp Thr Tyr Leu Glu Lys Leu Val Val Lys Phe Gly Asp Glu Ile Val
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Leu Asn Ala Gln Ile Glu Thr Pro Val Lys Asp Tyr Ala Gly Gly Lys
95 100 105

ttc ccc ggc gga ggg tca aaa gaa caa tcc gtt tct ttt ttg gaa ggg 869
Phe Pro Gly Gly Gly Ser Lys Glu Gln Ser Val Ser Phe Leu Glu Gly
110 115 120

ctt gaa gaa gct gaa atc gcc ggc cgc gag gtg acg gtt caa ttg gat 917
Leu Glu Glu Ala Glu Ile Ala Gly Arg Glu Val Thr Val Gln Leu Asp
125 130 135

tgg aga gag ggc aaa caa gcg tcc cat aca gga ttt acg ctt gat aaa 965
Trp Arg Glu Gly Lys Gln Ala Ser His Thr Gly Phe Thr Leu Asp Lys
140 145 150 155

agc tca tgg taaaaggcgg aatatcgatt atattccgcc tacctcaatt 1014
Ser Ser Trp

ttgcttcgca tcgtcagctc ttctgcggc cccaaatccc gaaatccggt cacactcttc 1074
ggaagggttca cgttcggtgc attcgatc caagtgtatg gctcaataca aagcagatca 1134
tcctgatcag atgtaccgtt aaacacaacc cagtgcctaa aatggccgct gcattgatag 1194
cgtacgcgaa tgccggcgag gctgtccgca atgacggcgg tgctgtttcc ttcttggctc 1254
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<210> 128
<211> 158
<212> PRT
<213> Bacillus licheniformis

<400> 128

Met Lys Gln Glu Tyr Lys Arg Pro Val Leu Phe Ile Ala Ser Leu Phe
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Met Ala Phe Cys Ala Val Tyr Phe Gly Gly Arg Leu Ile Gly Phe Tyr
20 25 30

Met Ala Glu Tyr Pro Lys Trp Asn Gly Gln Ser Ala Asp Gly Asn Trp
35 40 45

Glu Ala Val Ile Lys Lys Ile Asp Gly Arg Ala Leu Phe Gly Gly Glu
50 55 60

Leu Tyr Trp Thr Gly Asp Arg Gly Lys Leu Asp Asp Thr Tyr Leu Glu
65 70 75 80

Lys Leu Val Val Lys Phe Gly Asp Glu Ile Val Leu Asn Ala Gln Ile
85 90 95

Glu Thr Pro Val Lys Asp Tyr Ala Gly Gly Lys Phe Pro Gly Gly Gly
100 105 110

Ser Lys Glu Gln Ser Val Ser Phe Leu Glu Gly Leu Glu Glu Ala Glu
115 120 125

Ile Ala Gly Arg Glu Val Thr Val Gln Leu Asp Trp Arg Glu Gly Lys
130 135 140

Gln Ala Ser His Thr Gly Phe Thr Leu Asp Lys Ser Ser Trp
145 150 155

<210> 129

<211> 1219

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (812)..(1114)

<223>

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ataaaaaatg cacgaaatgg ggacaaatca g atg aaa cgt gtc att gtg ctg 832
Met Lys Arg Val Ile Val Leu
1 5

ttt tcg att ttg ctc gcc ctg ttc att gtt tat tat gac ttg aaa tca 880
Phe Ser Ile Leu Leu Ala Leu Phe Ile Val Tyr Tyr Asp Leu Lys Ser
10 15 20

ggc acc atc cct caa aac gcc tta ccg gct tca acc atg gca gcg gaa 928
Gly Thr Ile Pro Gln Asn Ala Leu Pro Ala Ser Thr Met Ala Ala Glu
25 30 35

gct ccg gct gca agc ctg caa tat aag tcc gtt acg gta aag ccc gga 976
Ala Pro Ala Ala Ser Leu Gln Tyr Lys Ser Val Thr Val Lys Pro Gly
40 45 50 55

caa acg gta ttt tca atc atc ggg aac agc gcc gtt ccg gct gac aaa 1024
Gln Thr Val Phe Ser Ile Ile Gly Asn Ser Ala Val Pro Ala Asp Lys
60 65 70

ata gcc gaa gat ttt gaa gag ttg aat ccg aat gtt gag gcg ggc cgc 1072
Ile Ala Glu Asp Phe Glu Glu Leu Asn Pro Asn Val Glu Ala Gly Arg
75 80 85

att caa gca ggt gtc acc tac aag ttt ccc gtt tat cct gat 1114
Ile Gln Ala Gly Val Thr Tyr Lys Phe Pro Val Tyr Pro Asp
90 95 100

taagcgtaa tttcttgatca gtttcatgaa cgggctgta caataagact tgtaaacgat 1174
ttggtataag aaaaggagca accgcctccg aattatactt aagga 1219

<210> 130

<211> 101

<212> PRT

<213> Bacillus licheniformis

<400> 130

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Val Tyr Tyr Asp Leu Lys Ser Gly Thr Ile Pro Gln Asn Ala Leu Pro
20 25 30

Ala Ser Thr Met Ala Ala Glu Ala Pro Ala Ala Ser Leu Gln Tyr Lys
35 40 45

Ser Val Thr Val Lys Pro Gly Gln Thr Val Phe Ser Ile Ile Gly Asn
50 55 60

Ser Ala Val Pro Ala Asp Lys Ile Ala Glu Asp Phe Glu Glu Leu Asn
65 70 75 80

10294.000.ST25.txt

Pro Asn Val Glu Ala Gly Arg Ile Gln Ala Gly Val Thr Tyr Lys Phe
85 90 95

Pro Val Tyr Pro Asp
100

<210> 131
<211> 1381
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(878)
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<400> 131
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Met Lys Phe Ser Lys Ile Gly Ala Leu Leu Leu
1 5 10
act ttg gcg tgt ttg ctt ttg cct ttt tct tcg gcg act gca gca ggt 581
Thr Leu Ala Cys Leu Leu Leu Pro Phe Ser Ser Ala Thr Ala Ala Gly
15 20 25
gcc ggt gta tgg gat aat atc ggc aca tac ggc atg acg tcg caa act 629
Ala Gly Val Trp Asp Asn Ile Gly Thr Tyr Gly Met Thr Ser Gln Thr
30 35 40
ccg atc atc aaa tca agc gga ggg gaa ttt tat ttt cac aac aac agc 677
Pro Ile Ile Lys Ser Ser Gly Gly Glu Phe Tyr Phe His Asn Asn Ser
45 50 55
ttt tac ggc ttt aca ttt acg ctg tat gaa gtt gac ggg gcg gga agc 725
Phe Tyr Gly Phe Thr Phe Thr Leu Tyr Glu Val Asp Gly Ala Gly Ser
60 65 70 75
acg cct gaa atc gca aga aaa aat ttc tac gtc gga ccg aaa agc aac 773
Thr Pro Glu Ile Ala Arg Lys Asn Phe Tyr Val Gly Pro Lys Ser Asn
80 85 90

10294.000.ST25.txt

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agt ccg gcg atc gat gtc agc agt ttt gca gat ggt gcg aat aaa caa      821
Ser Pro Ala Ile Asp Val Ser Ser Phe Ala Asp Gly Ala Asn Lys Gln
          95                      100                      105

gca gaa ctc gtc ctg ttt aaa ggg aat gat aca tat atc acc gtt act      869
Ala Glu Leu Val Leu Phe Lys Gly Asn Asp Thr Tyr Ile Thr Val Thr
          110                      115                      120

tgt tat gat tgaatgtccc ataaacagca agccccccgt ttacagccgg      918
Cys Tyr Asp

cgggtttttt tgatcaagtt ccttccttat acctataggc acaaaaaagt gcctatatga      978
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accaaacaat agacgaattg aaaggccaat ttcccagggc tgttcttcaa gcggcccctt      1278
atgaccttgg cactgaaaaa ggggtgtcaa gcctatttagc agcattcccc gatgttgata      1338
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<210> 132

<211> 126

<212> PRT

<213> Bacillus licheniformis

<400> 132

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          20          25          30

Asn Ile Gly Thr Tyr Gly Met Thr Ser Gln Thr Pro Ile Ile Lys Ser
          35          40          45

Ser Gly Gly Glu Phe Tyr Phe His Asn Asn Ser Phe Tyr Gly Phe Thr
          50          55          60

Phe Thr Leu Tyr Glu Val Asp Gly Ala Gly Ser Thr Pro Glu Ile Ala
65          70          75          80

Arg Lys Asn Phe Tyr Val Gly Pro Lys Ser Asn Ser Pro Ala Ile Asp
          85          90          95

Val Ser Ser Phe Ala Asp Gly Ala Asn Lys Gln Ala Glu Leu Val Leu
          100          105          110

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Phe Lys Gly Asn Asp Thr Tyr Ile Thr Val Thr Cys Tyr Asp
 115 120 125

<210> 133

<211> 1581

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (601)..(978)

<223>

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 gttctcactg gctaaccgga tcaaatgata ttcaggagtc agcataatac atccagttca 180
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 atg aaa aat cat ttg tat gag aaa aaa aag agg aaa cct ttg act cgg 648
 Met Lys Asn His Leu Tyr Glu Lys Lys Lys Arg Lys Pro Leu Thr Arg
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 aca att aaa gcg acg ctc gcc gtg ttg aca atg tcc atc gct ttg gtg 696
 Thr Ile Lys Ala Thr Leu Ala Val Leu Thr Met Ser Ile Ala Leu Val
 20 25 30
 gga ggc gct acg gtg cct tca ttt gca tgg gtg aat ccg ggt tat cac 744
 Gly Gly Ala Thr Val Pro Ser Phe Ala Trp Val Asn Pro Gly Tyr His
 35 40 45
 tac cag tac cca tcg gaa ggt ggt aca tgg agg tat gga ttc gta aac 792
 Tyr Gln Tyr Pro Ser Glu Gly Gly Thr Trp Arg Tyr Gly Phe Val Asn
 50 55 60
 gcc ggg ctc cgt tca gag tac aac cac ccg aca aag gtc cac ggc tcg 840
 Ala Gly Leu Arg Ser Glu Tyr Asn His Pro Thr Lys Val His Gly Ser
 65 70 75 80
 aca gtg caa aag ctc atc gat gga aaa gtg gat aaa acg aat aga agt 888
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10294.000.ST25.txt

Thr	Val	Gln	Lys	Leu	Ile	Asp	Gly	Lys	Val	Asp	Lys	Thr	Asn	Arg	Ser	
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Ile	Asp	Thr	Ala	Ala	Gly	Arg	Tyr	Ser	Asn	Ala	Tyr	Val	Gly	Ala	Ile	
			100					105					110			
aac	tca	cct	ggt	ctt	aag	ggt	cgt	tac	tac	tat	cg	acc	aac			978
Asn	Ser	Pro	Gly	Leu	Lys	Gly	Arg	Tyr	Tyr	Tyr	Arg	Thr	Asn			
		115					120					125				
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tgctttcgg	gtactgccaa	agcatctcca	caaaagatag	tgcatatctg	caggaaaaaa											1518
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tct																1581

<210> 134

<211> 126

<212> PRT

<213> Bacillus licheniformis

<400> 134

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			20					25					30			
Gly	Gly	Ala	Thr	Val	Pro	Ser	Phe	Ala	Trp	Val	Asn	Pro	Gly	Tyr	His	
		35					40				45					
Tyr	Gln	Tyr	Pro	Ser	Glu	Gly	Gly	Thr	Trp	Arg	Tyr	Gly	Phe	Val	Asn	
	50					55					60					
Ala	Gly	Leu	Arg	Ser	Glu	Tyr	Asn	His	Pro	Thr	Lys	Val	His	Gly	Ser	
65					70					75					80	
Thr	Val	Gln	Lys	Leu	Ile	Asp	Gly	Lys	Val	Asp	Lys	Thr	Asn	Arg	Ser	
				85					90					95		

Ile Asp Thr Ala Ala Gly Arg Tyr Ser Asn Ala Tyr Val Gly Ala Ile
 100 105 110

Asn Ser Pro Gly Leu Lys Gly Arg Tyr Tyr Tyr Arg Thr Asn
 115 120 125

<210> 135

<211> 1357

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(854)

<223>

<400> 135
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 gaaaattaga attgaagggtg atg aac gtg gaa att gct atc att gcg ctg ctc 533
 Met Asn Val Glu Ile Ala Ile Ile Ala Leu Leu
 1 5 10
 gtt gtc agt att gcg ctg att gca ttc tca tat ttt caa aga gaa ccg 581
 Val Val Ser Ile Ala Leu Ile Ala Phe Ser Tyr Phe Gln Arg Glu Pro
 15 20 25
 atc aag gaa gtt gaa cag gag ttg gaa acc ctt cag ctg tcc gcc atg 629
 Ile Lys Glu Val Glu Gln Glu Leu Glu Thr Leu Gln Leu Ser Ala Met
 30 35 40
 cag gaa atc tat aaa ctg aaa aag aag atg acc gtg ctt gag gaa gag 677
 Gln Glu Ile Tyr Lys Leu Lys Lys Lys Met Thr Val Leu Glu Glu Glu
 45 50 55
 ctc ctc gat tca aat gtg gtc gtc cgc aga ccg aat gcc gga atc agc 725
 Leu Leu Asp Ser Asn Val Val Val Arg Arg Pro Asn Ala Gly Ile Ser
 60 65 70 75
 cag cat att gcg aag cag att ctt tca aaa tat caa aac ggc atg tct 773

Gln His Ile Ala Lys Gln Ile Leu Ser Lys Tyr Gln Asn Gly Met Ser
80 85 90

gta gac gcc atc gca aaa gct gag cac gta tct gtc gaa gat gtc aaa 821
Val Asp Ala Ile Ala Lys Ala Glu His Val Ser Val Glu Asp Val Lys
95 100 105

gcg atc att aaa gac tat gag agg gtg ctt gta tgaccagaca gagtgtaaa 874
Ala Ile Ile Lys Asp Tyr Glu Arg Val Leu Val
110 115

gcatttgccc ggagaatgga ttgtggctac cgccgttctt gcaagcgcat tttatttgaa 934
cggataatac gacccgattt acctgtgcga tgcgaagatt ctccgtcagc atcagactgt 994
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gattgatgat aaaatcaggc aggtggaggt tttctaaaaa cgctcttgag accgcctcac 1234
cggtgcgttc ctggttcata aagtttcccc agcgtccgat cgcttgacca agcagaatgc 1294
ttggagcagc gatatcagcc agcttccaaa acgaaagccc cttgactttc gcataaatga 1354
ttc 1357

<210> 136

<211> 118

<212> PRT

<213> Bacillus licheniformis

<400> 136

Met Asn Val Glu Ile Ala Ile Ile Ala Leu Leu Val Val Ser Ile Ala
1 5 10 15

Leu Ile Ala Phe Ser Tyr Phe Gln Arg Glu Pro Ile Lys Glu Val Glu
20 25 30

Gln Glu Leu Glu Thr Leu Gln Leu Ser Ala Met Gln Glu Ile Tyr Lys
35 40 45

Leu Lys Lys Lys Met Thr Val Leu Glu Glu Glu Leu Leu Asp Ser Asn
50 55 60

Val Val Val Arg Arg Pro Asn Ala Gly Ile Ser Gln His Ile Ala Lys
65 70 75 80

Gln Ile Leu Ser Lys Tyr Gln Asn Gly Met Ser Val Asp Ala Ile Ala
85 90 95

Lys Ala Glu His Val Ser Val Glu Asp Val Lys Ala Ile Ile Lys Asp
100 105 110

Tyr Glu Arg Val Leu Val
115

<210> 137

<211> 1297

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(794)

<223>

<400> 137
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ttcttaaacy ttgatatgac gcagttttta cgaagattta accgtcgaat tttcgacctg 180
tttctaacga atagttttatc gtaattccga tgaatttttc gcccattattg cgatgaaatt 240
gtgctacgat ccgaagggtt taatacagta tttgaagggtc ctcgttttta taaacgaggc 300
cgtttttttg cccgcaaagt tactgtttgc gatgtaagat caaaaagggtg aatcatttca 360
gcacagtgtg tattgtgtaa agtcattccta aaagcttattc tattgattcc gaaatattgt 420
aatttgtaca ctttttggac atacctgcat gttatatgat gaaatagaaa tgaaataaat 480
ggaaaaggag ttgttttaaa atg aag gtc aat aaa tta tta act ggt acg act 533
Met Lys Val Asn Lys Leu Leu Thr Gly Thr Thr
1 5 10
ctg gct gtt ggt tta ctt att tct gca gcg ccg gta ttt gct gca tcg 581
Leu Ala Val Gly Leu Leu Ile Ser Ala Ala Pro Val Phe Ala Ala Ser
15 20 25
cat tca tct gag gtg att gca cat ccg act gct caa tat atc aat tgt 629
His Ser Ser Glu Val Ile Ala His Pro Thr Ala Gln Tyr Ile Asn Cys
30 35 40
cca agt gac ttg cca agc tca ttc aaa agc agt aaa tca tca aaa tgt 677
Pro Ser Asp Leu Pro Ser Ser Phe Lys Ser Ser Lys Ser Ser Lys Cys
45 50 55
gta aaa tca tct tct gga gtt ttc agt aac aaa ttt tct gat agc gat 725
Val Lys Ser Ser Ser Gly Val Phe Ser Asn Lys Phe Ser Asp Ser Asp
60 65 70 75
gga aca tgg tat ttc aaa ggg aaa ttt tac agt aat gtt ttt aat act 773
Gly Thr Trp Tyr Phe Lys Gly Lys Phe Tyr Ser Asn Val Phe Asn Thr
80 85 90
tgg gtt ggt ttt tat gaa gga tgaacaaaa aaggggggct cccctttttt 824

Trp Val Gly Phe Tyr Glu Gly
95

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gctcatcgta	aacagcaatg	caaaaatagg	tgcaaactgt	gacattcatc	aaggggttaa	1064
tatcggacaa	aatcacgctc	gccgcgatgt	tcccacaatc	ggagacaatg	tctggatcgg	1124
gccgggggca	aagctctttg	gcgacattca	cattgctgac	ggcatatcaa	ttggcgcaaa	1184
cgccgtggtc	aacaaatctt	tcactgagga	aaatattaca	atagccggca	tgccctgcca	1244
aaagattaaa	gaggcgccgt	caaataaaga	ccggaagcaa	gctgttcagc	ggc	1297

<210> 138

<211> 98

<212> PRT

<213> Bacillus licheniformis

<400> 138

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Leu	Ile	Ser	Ala	Ala	Pro	Val	Phe	Ala	Ala	Ser	His	Ser	Ser	Glu	Val
			20					25					30		
Ile	Ala	His	Pro	Thr	Ala	Gln	Tyr	Ile	Asn	Cys	Pro	Ser	Asp	Leu	Pro
		35					40				45				
Ser	Ser	Phe	Lys	Ser	Ser	Lys	Ser	Ser	Lys	Cys	Val	Lys	Ser	Ser	Ser
	50					55					60				
Gly	Val	Phe	Ser	Asn	Lys	Phe	Ser	Asp	Ser	Asp	Gly	Thr	Trp	Tyr	Phe
65					70				75						80
Lys	Gly	Lys	Phe	Tyr	Ser	Asn	Val	Phe	Asn	Thr	Trp	Val	Gly	Phe	Tyr
				85					90					95	
Glu	Gly														

<210> 139

<211> 1261

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(836)

<223>

<400> 139

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caaggctgat tgtagggacg tcgatcggca catcggcagc gattgttccc ttgacttttt      120
atgcgggggcc ttacatcgct agactcgtcg agaactctct gcttgaagtg gatccgggag      180
tcattgaagc cgctgaagca atgggagcga ctccgagaca gatcatcttc aggtttctga      240
ttccagaagc gctcggttcg cttgtgctga gttttacggg ggcaacgggc ggattggctg      300
gggcgtcggc gatggctggg gcgattggg caggcgggtct tggggatttg gcgatcacat      360
acggctatca aagatttgac acgctgacga tgatcatcac ggttgcaatt ctcgatcatcg      420
tagtgcaagg attgcagaca tccggaaacg ttctgtcaaa aaaattgaga agaagataga      480
cagagaggga gacggctatt atg aaa aaa ttt gca tgt gtt gtg atc ttc ctg      533
                      Met Lys Lys Phe Ala Cys Val Val Ile Phe Leu
                      1       5       10

ctg ctt gcg gca gtg atc gcg ggg tgc gcg gca gac tct gat gcg aaa      581
Leu Leu Ala Ala Val Ile Ala Gly Cys Ala Ala Asp Ser Asp Ala Lys
                      15       20       25

acc att aaa atc ggc atc agc gga acg gat acg aga att tgg gac ttt      629
Thr Ile Lys Ile Gly Ile Ser Gly Thr Asp Thr Arg Ile Trp Asp Phe
                      30       35       40

gtg aag aaa aaa gcc gaa aaa gaa ggc tta aag ctt gaa atc gtc aaa      677
Val Lys Lys Lys Ala Glu Lys Glu Gly Leu Lys Leu Glu Ile Val Lys
                      45       50       55

tac tcc gac tat gtt cag cca aac cag gct ttg gcg agc ggc gac att      725
Tyr Ser Asp Tyr Val Gln Pro Asn Gln Ala Leu Ala Ser Gly Asp Ile
60                      65                      70                      75

gac cgc caa cgc ttt tca gac gat atc cta ctt tca tgc att caa aaa      773
Asp Arg Gln Arg Phe Ser Asp Asp Ile Leu Leu Ser Cys Ile Gln Lys
80                      85                      90

gga acg caa cct tta att atc gcc ggt cgg cac aac gac acc agg tcg      821
Gly Thr Gln Pro Leu Ile Ile Ala Gly Arg His Asn Asp Thr Arg Ser
95                      100                      105

ggg ggg gga gga aga ataaataaac acgggccctt ttggttgata agtccccggc      876
Gly Gly Gly Gly Arg
110

attacaagcc cgaccattcc cattgctgat ccgcgttttt cctttgggaa aatcaataaa      936
agcaccgtct gcatcaatgg catcataatg ccggcgccag ccgcctgcac gacgcgcccc      996
gcaatcagcg ccggaaagct gaatgacaag gcgcagatca gcgtgccggc cgtaaataaa      1056
gacattgccg ccatgaacag ctttctcggt gtgaattttt caattaaata agccgtaact      1116

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ggaatcatga tcccattcac gagcataaaa acggtcgtca gccattgggc aagccccggc 1176
gtaatgttta agtccctcat aatcggaggc agagccctga tgaatcccct aatgattttg 1236
gtaaaaatca ttaagttaag gtgga 1261

<210> 140

<211> 112

<212> PRT

<213> Bacillus Ticheniformis

<400> 140

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Ile Ala Gly Cys Ala Ala Asp Ser Asp Ala Lys Thr Ile Lys Ile Gly
20 25 30

Ile Ser Gly Thr Asp Thr Arg Ile Trp Asp Phe Val Lys Lys Lys Ala
35 40 45

Glu Lys Glu Gly Leu Lys Leu Glu Ile Val Lys Tyr Ser Asp Tyr Val
50 55 60

Gln Pro Asn Gln Ala Leu Ala Ser Gly Asp Ile Asp Arg Gln Arg Phe
65 70 75 80

Ser Asp Asp Ile Leu Leu Ser Cys Ile Gln Lys Gly Thr Gln Pro Leu
85 90 95

Ile Ile Ala Gly Arg His Asn Asp Thr Arg Ser Gly Gly Gly Gly Arg
100 105 110

<210> 141

<211> 1426

<212> DNA

<213> Bacillus Ticheniformis

<220>

<221> CDS

<222> (507)..(923)

<223>

10294.000.ST25.txt

<400> 141

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gccgccgtct ccgccgccga ccacaagcac atgctcagga ttcggatgcg taaacagggg      180
cacgtgcgcc accatttcgt ggtagacaaa ttcatctttt tcagatgtca tgaccatgcc      240
gtccaaaaac agcatgttgc cgaattcttc agtctcggcc atttcgagct tttgaaaatc      300
tgtctgctct gtatgtaaag tcctgttgat tttcattgta ataccgaaat ttttcgtttg      360
cttctctgta taccaaagtc cgctcaaagc gtcattcttc tttcgtgata agctgtattt      420
caatctatct tttctgcctg cggcggcgat tattctgcac tgaagcatcg gcttttgcct      480
aaggaaaaag tatagaggaa ttgcag gtg att gta aag acg gat cga ttc att      533
                        Val Ile Val Lys Thr Asp Arg Phe Ile
                        1                    5

ttc acg agt cat tcc aag tcc att ata ttc cca atc gcc agt ttt tct      581
Phe Thr Ser His Ser Lys Ser Ile Ile Phe Pro Ile Ala Ser Phe Ser
10                        15                        20                        25

ttt ata ttg gct aag cta agc aca gat gtg cat acc tgt gcg ctt ttg      629
Phe Ile Leu Ala Lys Leu Ser Thr Asp Val His Thr Cys Ala Leu Leu
30                        35                        40

gag gtg tgc tca ttt gca gag cac tca act gct caa att gta tat atc      677
Glu Val Cys Ser Phe Ala Glu His Ser Thr Ala Gln Ile Val Tyr Ile
45                        50                        55

ctc ccg ccg gaa cag gct ttt att gac ctt ttt tct gat ccg acc ggc      725
Leu Pro Pro Glu Gln Ala Phe Ile Asp Leu Phe Ser Asp Pro Thr Gly
60                        65                        70

cgt ttt gtc ttt cac ccc cgt tca tat ccg gga cgc tgc cct tcc ccc      773
Arg Phe Val Phe His Pro Arg Ser Tyr Pro Gly Arg Cys Pro Ser Pro
75                        80                        85

tct ccc gga tcg gcc ttc tcg aaa ttc agc gga ttt gct tat ttg atg      821
Ser Pro Gly Ser Ala Phe Ser Lys Phe Ser Gly Phe Ala Tyr Leu Met
90                        95                        100                        105

cct atg gtc tct cgc tct cgt ccc tat gct gtt gtt tta cgt tac ttc      869
Pro Met Val Ser Arg Ser Arg Pro Tyr Ala Val Val Leu Arg Tyr Phe
110                        115                        120

aaa tgt ctg ccg ggc tct ccg cgt ccc acg cca cca aac aaa cgg ggt      917
Lys Cys Leu Pro Gly Ser Pro Arg Pro Thr Pro Pro Asn Lys Arg Gly
125                        130                        135

ctc ccc tgattttcgt cggctgcccc tctctgcttt ttgattaccc cccttctctt      973
Leu Pro

attgaagccc gcctcggctg gtttccatcg tccgctacgc gccgcaaag ttatgctttt      1033
ctttatctaa aggctctacc cttagtatct aactaacacc tgcattgcaca gaaatcggag      1093
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tgcattgcacc gatatcggag tggctctgtg catgcaccga tatcggagtg gctctcatgc      1273
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10294.000.ST25.txt

gaatgcggcc catgtacgtg ttgatgaatg cggccattct tatcagggga cccaacggg 1393
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<210> 142

<211> 139

<212> PRT

<213> Bacillus licheniformis

<400> 142

Val Ile Val Lys Thr Asp Arg Phe Ile Phe Thr Ser His Ser Lys Ser
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Ile Ile Phe Pro Ile Ala Ser Phe Ser Phe Ile Leu Ala Lys Leu Ser
20 25 30

Thr Asp Val His Thr Cys Ala Leu Leu Glu Val Cys Ser Phe Ala Glu
35 40 45

His Ser Thr Ala Gln Ile Val Tyr Ile Leu Pro Pro Glu Gln Ala Phe
50 55 60

Ile Asp Leu Phe Ser Asp Pro Thr Gly Arg Phe Val Phe His Pro Arg
65 70 75 80

Ser Tyr Pro Gly Arg Cys Pro Ser Pro Ser Pro Gly Ser Ala Phe Ser
85 90 95

Lys Phe Ser Gly Phe Ala Tyr Leu Met Pro Met Val Ser Arg Ser Arg
100 105 110

Pro Tyr Ala Val Val Leu Arg Tyr Phe Lys Cys Leu Pro Gly Ser Pro
115 120 125

Arg Pro Thr Pro Pro Asn Lys Arg Gly Leu Pro
130 135

<210> 143

<211> 1513

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (496)..(1035)

<223>

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 aacaatgccc agtCaggagg tgatgaatga tgccatggat gtttttagtg atttccggaa 180
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 agatgctatc agCCggtgtt gcatatgccg tatggaccgg aatcggcagc atcggcatta 360
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 gctttattat aatCgggggtg atcggcctgc gccttacatc atcttaaatt ttaatttgca 480
 ttggaggttg ctgat atg att aat cag ctt aaa ttg cgt ccg ctt gaa aga 531
 Met Ile Asn Gln Leu Lys Leu Arg Pro Leu Glu Arg
 1 5 10
 gaa gac ctt ccg ttt gtc cac cgt ctt aac aac gat gcg aaa att atg 579
 Glu Asp Leu Pro Phe Val His Arg Leu Asn Asn Asp Ala Lys Ile Met
 15 20 25
 tca tat tgg ttt gaa gaa ccg tac gag act ttt gtt gag ctg cag gat 627
 Ser Tyr Trp Phe Glu Glu Pro Tyr Glu Thr Phe Val Glu Leu Gln Asp
 30 35 40
 tta ttt gac aaa cac att cac gac caa agc gag cgg cgc ttt atc ata 675
 Leu Phe Asp Lys His Ile His Asp Gln Ser Glu Arg Arg Phe Ile Ile
 45 50 55 60
 gag aaa gag act gag atg atc gga ttg gta gag ctg gtc gaa att gat 723
 Glu Lys Glu Thr Glu Met Ile Gly Leu Val Glu Leu Val Glu Ile Asp
 65 70 75
 tat att cac agg cgg gcg gag ttt caa atc ata att gat ccc gag cat 771
 Tyr Ile His Arg Arg Ala Glu Phe Gln Ile Ile Ile Asp Pro Glu His
 80 85 90
 caa ggg aac ggt tat tcg tca agc gca aca tat ttg gca atg aac tac 819
 Gln Gly Asn Gly Tyr Ser Ser Ser Ala Thr Tyr Leu Ala Met Asn Tyr
 95 100 105
 gca ttt tcc gtc ttg aac ttg cac aaa ttg tat ttg atc gtc gac gaa 867
 Ala Phe Ser Val Leu Asn Leu His Lys Leu Tyr Leu Ile Val Asp Glu
 110 115 120
 gat aat gca aaa gcg att cac ttg tat aaa aag gca ggg ttc act atc 915
 Asp Asn Ala Lys Ala Ile His Leu Tyr Lys Lys Ala Gly Phe Thr Ile
 125 130 135 140
 gag agc gag ctg cag gat gaa ttt ttc gtc gac ggc tat tat cgt aac 963
 Glu Ser Glu Leu Gln Asp Glu Phe Phe Val Asp Gly Tyr Tyr Arg Asn
 145 150 155
 gcc att aga atg tgc att ttt cag gat gag ttt tta tca ctt aaa aaa 1011
 Ala Ile Arg Met Cys Ile Phe Gln Asp Glu Phe Leu Ser Leu Lys Lys
 160 165 170
 agc aaa gag gaa ggc atg cag gga taaataaaag agatggcggc gccatctcct 1065

10294.000.ST25.txt

Ser Lys Glu Glu Gly Met Gln Gly
175 180

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aaaaaaattg aataacgtga catgaaca 1513

<210> 144
<211> 180
<212> PRT
<213> Bacillus licheniformis

<400> 144

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20 25 30

Glu Glu Pro Tyr Glu Thr Phe Val Glu Leu Gln Asp Leu Phe Asp Lys
35 40 45

His Ile His Asp Gln Ser Glu Arg Arg Phe Ile Ile Glu Lys Glu Thr
50 55 60

Glu Met Ile Gly Leu Val Glu Leu Val Glu Ile Asp Tyr Ile His Arg
65 70 75 80

Arg Ala Glu Phe Gln Ile Ile Ile Asp Pro Glu His Gln Gly Asn Gly
85 90 95

Tyr Ser Ser Ser Ala Thr Tyr Leu Ala Met Asn Tyr Ala Phe Ser Val
100 105 110

Leu Asn Leu His Lys Leu Tyr Leu Ile Val Asp Glu Asp Asn Ala Lys
115 120 125

Ala Ile His Leu Tyr Lys Lys Ala Gly Phe Thr Ile Glu Ser Glu Leu
130 135 140

10294.000.ST25.txt

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cta tca gct tca tgg gca gag cgc cac ccg gat gtc gta gaa aga atc Leu Ser Ala Ser Trp Ala Glu Arg His Pro Asp Val Val Glu Arg Ile 95 100 105	820
cgt aaa gat ggt cac cag atc ggg agt atg ggc tat gct tat aaa aac Arg Lys Asp Gly His Gln Ile Gly Ser Met Gly Tyr Ala Tyr Lys Asn 110 115 120	868
tat tcg caa atg aag aaa agc gag atc aaa aaa gac tta gca aaa gca Tyr Ser Gln Met Lys Lys Ser Glu Ile Lys Lys Asp Leu Ala Lys Ala 125 130 135	916
cga cac tcc ttt caa aaa ctc ggg ctt gac gac ctt acg ctt tta aga Arg His Ser Phe Gln Lys Leu Gly Leu Asp Asp Leu Thr Leu Leu Arg 140 145 150	964
ccg ccg acc ggc cag ttt aat aaa gac gta ctc gat gtt gct aaa cag Pro Pro Thr Gly Gln Phe Asn Lys Asp Val Leu Asp Val Ala Lys Gln 155 160 165 170	1012
tac ggc tac acc gtt gtt cat tat agt att aac tcg gat gac tgg acg Tyr Gly Tyr Thr Val Val His Tyr Ser Ile Asn Ser Asp Asp Trp Thr 175 180 185	1060
aac ccg ggg gtt caa aag atc gtc caa aac gta aat gga acg gta aac Asn Pro Gly Val Gln Lys Ile Val Gln Asn Val Asn Gly Thr Val Asn 190 195 200	1108
gcc ggt gac atc gtg ctc ttt cac gct tca gat tcc gcc aaa caa aca Ala Gly Asp Ile Val Leu Phe His Ala Ser Asp Ser Ala Lys Gln Thr 205 210 215	1156
aaa gaa gcc ctg cca gag atc gtg cac cat ctc aga agc aag ggg ctc Lys Glu Ala Leu Pro Glu Ile Val His His Leu Arg Ser Lys Gly Leu 220 225 230	1204
aaa aac gta aca gtc agc gaa tta atc gca aat acg gat gca aaa tct Lys Asn Val Thr Val Ser Glu Leu Ile Ala Asn Thr Asp Ala Lys Ser 235 240 245 250	1252
tca gaa gta aag tagcagccgg tctaagcgcg tgcctgaaat tttggcagca Ser Glu Val Lys	1304
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ctaccgccaa aataaagagc ggcagccaaa tgtacggaat gatggagcct ccatcttttt	1544
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gaatcgaatt ccacaaagaa tgagatctga aaatttccag tgcaaagcgg tgaatcgta	1664
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<210> 146

<211> 254

<212> PRT

<213> *Bacillus licheniformis*

<400> 146

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 Asn Leu Leu Pro Leu Pro Val Phe Ser Thr Glu Gly Gly Ala Lys Ala
 35 40 45
 Val Tyr Arg Gly Asp Ser Asp Thr Asn Glu Val Ala Leu Thr Phe Asn
 50 55 60
 Ile Ser Trp Gly Asp Gln Lys Ala Met Pro Ile Leu Asp Thr Leu Lys
 65 70 75 80
 Ala Asn Gly Ile Lys Asp Ala Thr Phe Phe Leu Ser Ala Ser Trp Ala
 85 90 95
 Glu Arg His Pro Asp Val Val Glu Arg Ile Arg Lys Asp Gly His Gln
 100 105 110
 Ile Gly Ser Met Gly Tyr Ala Tyr Lys Asn Tyr Ser Gln Met Lys Lys
 115 120 125
 Ser Glu Ile Lys Lys Asp Leu Ala Lys Ala Arg His Ser Phe Gln Lys
 130 135 140
 Leu Gly Leu Asp Asp Leu Thr Leu Leu Arg Pro Pro Thr Gly Gln Phe
 145 150 155 160
 Asn Lys Asp Val Leu Asp Val Ala Lys Gln Tyr Gly Tyr Thr Val Val
 165 170 175
 His Tyr Ser Ile Asn Ser Asp Asp Trp Thr Asn Pro Gly Val Gln Lys
 180 185 190
 Ile Val Gln Asn Val Asn Gly Thr Val Asn Ala Gly Asp Ile Val Leu
 195 200 205
 Phe His Ala Ser Asp Ser Ala Lys Gln Thr Lys Glu Ala Leu Pro Glu
 210 215 220
 Ile Val His His Leu Arg Ser Lys Gly Leu Lys Asn Val Thr Val Ser
 225 230 235 240

Glu Leu Ile Ala Asn Thr Asp Ala Lys Ser Ser Glu Val Lys
 245 250

<210> 147

<211> 1855

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (480)..(1346)

<223>

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 acacgaggaa gacgcggaat aaggaggaa atagtgcgc aggggtgaacg gtagggaggg 180
 tggcaaatag tagtatgata tttgaaagac ggggtcccgt cgaatcggt gaaaaacaaa 240
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 ctggaccgcg ataaagacaa aattgcctgt gagcgctgat atatccaaaa aaagatctct 360
 gccaaaggat ctttttttgt ttatcaggaa atttatgaaa attaaagact gctgaaacat 420
 aatcttaaca gtgcgaacct atactttggc aagagaagag caaaagggga gtggatgat 479
 gtg tca gct tta ttc aaa aaa ttg atg tta tct tca ttg atc ggg gtt 527
 Val Ser Ala Leu Phe Lys Lys Leu Met Leu Ser Ser Leu Ile Gly Val
 1 5 10 15
 tcc atc ggg tca gcg ctg ttt gca ccg aat gcg ggt gca caa gag ccg 575
 Ser Ile Gly Ser Ala Leu Phe Ala Pro Asn Ala Gly Ala Gln Glu Pro
 20 25 30
 gcg gtg aag cct aaa aaa gtg gat gtc att gca cac aga ggc gct tcg 623
 Ala Val Lys Pro Lys Lys Val Asp Val Ile Ala His Arg Gly Ala Ser
 35 40 45
 gga tat gcg ccg gaa aac acg atg gct gct ttt gat aaa gcg ctt cag 671
 Gly Tyr Ala Pro Glu Asn Thr Met Ala Ala Phe Asp Lys Ala Leu Gln
 50 55 60
 atg aaa gca gat tat atc gag ctg gat gtt caa atg tcc aaa gac ggg 719
 Met Lys Ala Asp Tyr Ile Glu Leu Asp Val Gln Met Ser Lys Asp Gly
 65 70 75 80
 gag ctt gtc atc att cac gat acg acc gta aac cgt acg aca gat att 767
 Glu Leu Val Ile Ile His Asp Thr Thr Val Asn Arg Thr Thr Asp Ile
 85 90 95
 gac tca gtg ctg ccg gtt gcc gta aag gat ttg acg ctt gcc gag ctg 815

10294.000.ST25.txt

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Arg	Lys	Leu	Asp	Ala	Gly	Ser	Phe	Phe	Gly	Pro	Gln	Phe	Ala	Gly	Glu	
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Arg	Ile	Pro	Thr	Phe	Glu	Glu	Val	Leu	Asp	Arg	Tyr	Lys	Gly	Lys	Val	
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gga	atg	ctg	atc	gaa	ttg	aaa	gag	cct	gca	cgc	tat	ccg	gga	atc	gaa	959
Gly	Met	Leu	Ile	Glu	Leu	Lys	Glu	Pro	Ala	Arg	Tyr	Pro	Gly	Ile	Glu	
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Asn	Gly	Lys	Ile	Ile	Val	Gln	Ser	Phe	Asp	Phe	Asn	Ser	Val	Tyr	Lys	
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Ala	Ala	Asp	Leu	Thr	Asp	Ala	Lys	Leu	Lys	Glu	Phe	Ser	Gly	Tyr	Ala	
	210					215					220					
aaa	tac	gtg	aac	gcc	aac	ttg	aaa	aat	gtg	gcc	gct	gat	cct	acg	ctt	1199
Lys	Tyr	Val	Asn	Ala	Asn	Leu	Lys	Asn	Val	Ala	Ala	Asp	Pro	Thr	Leu	
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gtg	ccg	aga	att	cat	gcg	ctc	ggc	atg	aag	ata	cgc	cct	tgg	acc	gtc	1247
Val	Pro	Arg	Ile	His	Ala	Leu	Gly	Met	Lys	Ile	Arg	Pro	Trp	Thr	Val	
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cgc	tcc	cgc	gat	gaa	gtg	cct	ccg	cta	ttt	agg	ccc	gcg	tgg	aac	ggg	1295
Arg	Ser	Arg	Asp	Glu	Val	Pro	Pro	Leu	Phe	Arg	Pro	Ala	Trp	Asn	Gly	
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att	gtg	aca	aac	ttt	ccc	gac	tat	tgt	tcc	aaa	aaa	gta	cgg	gag	ccc	1343
Ile	Val	Thr	Asn	Phe	Pro	Asp	Tyr	Cys	Ser	Lys	Lys	Val	Arg	Glu	Pro	
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Gln																
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<210> 148

<211> 289

<212> PRT

<213> Bacillus licheniformis

<400> 148

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35 40 45

Gly Tyr Ala Pro Glu Asn Thr Met Ala Ala Phe Asp Lys Ala Leu Gln
50 55 60

Met Lys Ala Asp Tyr Ile Glu Leu Asp Val Gln Met Ser Lys Asp Gly
65 70 75 80

Glu Leu Val Ile Ile His Asp Thr Thr Val Asn Arg Thr Thr Asp Ile
85 90 95

Asp Ser Val Leu Pro Val Ala Val Lys Asp Leu Thr Leu Ala Glu Leu
100 105 110

Arg Lys Leu Asp Ala Gly Ser Phe Phe Gly Pro Gln Phe Ala Gly Glu
115 120 125

Arg Ile Pro Thr Phe Glu Glu Val Leu Asp Arg Tyr Lys Gly Lys Val
130 135 140

Gly Met Leu Ile Glu Leu Lys Glu Pro Ala Arg Tyr Pro Gly Ile Glu
145 150 155 160

Gly Lys Val Ser Ala Ala Leu Lys Glu Arg Arg Met Asp Lys Pro Lys
165 170 175

Asn Gly Lys Ile Ile Val Gln Ser Phe Asp Phe Asn Ser Val Tyr Lys
180 185 190

Ile His Gln Leu Leu Pro Ser Met Pro Thr Gly Val Leu Thr Ser Lys
195 200 205

Ala Ala Asp Leu Thr Asp Ala Lys Leu Lys Glu Phe Ser Gly Tyr Ala
210 215 220

Lys Tyr Val Asn Ala Asn Leu Lys Asn Val Ala Ala Asp Pro Thr Leu
225 230 235 240

Val Pro Arg Ile His Ala Leu Gly Met Lys Ile Arg Pro Trp Thr Val
245 250 255

Arg Ser Arg Asp Glu Val Pro Pro Leu Phe Arg Pro Ala Trp Asn Gly
260 265 270

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၆၇၈

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<211> 2200

<212> DNA

<213> *Bacillus licheniformis*

<220>

<221> CDS

<222> (501)..(1697)

<223>

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gaagggatgc tccctcttga cgaatgggtc aattttgcag gcggtaatga aaactaccgg 180

gtatgggcgg ctttaagagga cggcaagcct gtcggcgttg tcatggttga agttgaggag 240

gacttgaccg qgaacattgc ccttttagtc gatccgtttt tgcgcggagg gggatatgga 300

aaagcgctca tcaaaaaggac gatggcattg ccggaaatga gccggatcaa caaatgggttc 360

gccggaattg aagaggataa caagaggtgc ttagcgtgct tccgatccgt cgggtattca 420

ttggaacacg aacagccgga cgaagactgc tactactctc ttattttattt cccggaatct 480

taaataagga gcataagaag atg aac ttg atc aaa tgg att ttg ttt tcc gtt 533
Met Asn Leu Ile Lys Trp Ile Leu Phe Ser Val
1 5 10

att tca ttc gcc ttt ttt cag ccg gca cca gcc gct cta tta aaa gaa 581
Ile Ser Phe Ala Phe Phe Gln Pro Ala Pro Ala Ala Leu Leu Lys Glu
15 20 25

aag gac gac tat act att ctt gtt tat atg att ggt tct gac atg gaa 629
Lys Asp Asp Tyr Thr Ile Leu Val Tyr Met Ile Gly Ser Asp Met Glu
30 35 40

10294.000.ST25.txt

agc Ser	gat Asp	ttt Phe	cat His	atg Met	gca Ala	agc Ser	gat Asp	gac Asp	att Ile	cag Gln	gaa Glu	atg Met	atg Met	gat Asp	gcg Ala	677
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ggt Gly	tca Ser	tct Ser	tca Ser	aac Asn	gtc Val	aat Asn	gtc Val	gtt Val	ctt Leu	cag Gln	aca Thr	gga Gly	gga Gly	gca Ala	aaa Lys	725
60					65					70					75	
aaa Lys	tgg Trp	gcg Ala	aac Asn	ccg Pro	tcg Ser	atc Ile	agt Ser	cac His	aag Lys	gtg Val	aat Asn	cag Gln	agg Arg	tgg Trp	aaa Lys	773
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aca Thr	tat Tyr	ccg Pro	gct Ala	aaa Lys	aaa Lys	tat Tyr	gta Val	ttg Leu	atc Ile	ttt Phe	tgg Trp	ggg Gly	cat His	ggg Gly	ctt Leu	917
	125					130					135					
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140					145					150					155	
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acg Thr	aag Lys	caa Gln	aag Lys	ttt Phe	gat Asp	tta Leu	atc Ile	ggt Gly	ttt Phe	gac Asp	aac Asn	tgc Cys	aaa Lys	atg Met	gcc Ala	1061
			175					180					185			
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		190					195					200				
gct Ala	tca Ser	gtc Val	gac Asp	tat Tyr	acg Thr	aat Asn	caa Gln	aac Asn	ggc Gly	tgg Trp	gat Asp	tat Tyr	aaa Lys	agg Arg	gcg Ala	1157
	205					210					215					
ctg Leu	cag Gln	tct Ser	gta Val	caa Gln	gac Asp	gac Asp	cct Pro	tca Ser	atc Ile	gat Asp	ccg Pro	aaa Lys	gag Glu	ctt Leu	ggc Gly	1205
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				240				245						250		
aca Thr	gaa Glu	gac Asp	ctg Leu	cag Gln	cag Gln	tct Ser	tta Leu	att Ile	caa Gln	ttg Leu	aac Asn	cgt Arg	gtc Val	aaa Lys	gac Asp	1301
			255					260					265			
gct Ala	gtc Val	gat Asp	gcc Ala	ctc Leu	gac Asp	aga Arg	ttg Leu	agc Ser	gta Val	aac Asn	atg Met	aac Asn	ctg Leu	gca Ala	ttg Leu	1349
		270					275					280				
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	285					290					295					
gaa Glu	gat Asp	tat Tyr	gca Ala	gat Asp	gaa Glu	tcg Ser	gat Asp	atg Met	gtt Val	gat Asp	ttg Leu	gcg Ala	gat Asp	ttg Leu	tca Ser	1445
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gta aaa tcc gtc aag aag gct gtc atc atg aac atc aaa tct ccg gag Val Lys Ser Val Lys Lys Ala Val Ile Met Asn Ile Lys Ser Pro Glu 335 340 345	1541
cat cca aga gga agc ggc atg tcc gtt tat tat ccg gcc aga gac aac His Pro Arg Gly Ser Gly Met Ser Val Tyr Tyr Pro Ala Arg Asp Asn 350 355 360	1589
cat aag cgg ttt gcg gaa aaa tcg aaa ata tac cgc ctg ctt gac ttc His Lys Arg Phe Ala Glu Lys Ser Lys Ile Tyr Arg Leu Leu Asp Phe 365 370 375	1637
agc agc cgg tat caa aca ttc atc aaa gat tac tcg cat tca aca ttt Ser Ser Arg Tyr Gln Thr Phe Ile Lys Asp Tyr Ser His Ser Thr Phe 380 385 390 395	1685
aac ttt gat cta tagttgcgtt taacagcaaa aaagcgccgg cggaataacc Asn Phe Asp Leu	1737
ggcacttttt ttatcggtc atgtgcttcc ggatcaatgg aagtcgtag atgatgaaag	1797
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cgtgtcaaaa aaaagcggaa tgaaacatca attgtgtcta attggagaat attttgtgaa	2097
cattctgtta cttttattat accacgttct tcgaaaaatg atacatactg gaaagcattt	2157
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<210> 150

<211> 399

<212> PRT

<213> Bacillus licheniformis

<400> 150

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Phe Gln Pro Ala Pro Ala Ala Leu Leu Lys Glu Lys Asp Asp Tyr Thr 20 25 30
Ile Leu Val Tyr Met Ile Gly Ser Asp Met Glu Ser Asp Phe His Met 35 40 45
Ala Ser Asp Asp Ile Gln Glu Met Met Asp Ala Gly Ser Ser Ser Asn 50 55 60

Val Asn Val Val Leu Gln Thr Gly Gly Ala Lys Lys Trp Ala Asn Pro
 65 70 75 80
 Ser Ile Ser His Lys Val Asn Gln Arg Trp Lys Val Glu His Gln Lys
 85 90 95
 Leu Val Pro Leu Glu Asn Val Gly Lys Lys Asn Met Asp Ser Pro Gly
 100 105 110
 Ser Val Thr Asp Phe Ile Thr Trp Gly Val Lys Thr Tyr Pro Ala Lys
 115 120 125
 Lys Tyr Val Leu Ile Phe Trp Gly His Gly Leu Gly Ser Val Asp Gly
 130 135 140
 Tyr Gly Gly Asp Glu Asn Phe Gly Asn Lys Lys Met Lys Ile Ser Glu
 145 150 155 160
 Leu Gln Ser Gly Ile Lys Thr Ala Tyr Glu His Thr Lys Gln Lys Phe
 165 170 175
 Asp Leu Ile Gly Phe Asp Asn Cys Lys Met Ala Gly Ile Glu Thr Ala
 180 185 190
 Tyr Ala Leu Arg Asp Tyr Gly Lys Tyr Met Leu Ala Ser Val Asp Tyr
 195 200 205
 Thr Asn Gln Asn Gly Trp Asp Tyr Lys Arg Ala Leu Gln Ser Val Gln
 210 215 220
 Asp Asp Pro Ser Ile Asp Pro Lys Glu Leu Gly Arg Glu Ile Ala Ala
 225 230 235 240
 Gly Tyr Val Gln Gln Ser Lys Glu Asn Gly Glu Thr Glu Asp Leu Gln
 245 250 255
 Gln Ser Leu Ile Gln Leu Asn Arg Val Lys Asp Ala Val Asp Ala Leu
 260 265 270
 Asp Arg Leu Ser Val Asn Met Asn Leu Ala Leu Lys Glu Pro Asp Gly
 275 280 285
 Lys Arg Leu Leu His Tyr Ala Arg Leu Ala Ala Glu Asp Tyr Ala Asp
 290 295 300
 Glu Ser Asp Met Val Asp Leu Ala Asp Leu Ser Ser Leu Ile Gly Gln
 305 310 315 320
 Gln Ile Gly Ala Glu Lys Glu Ala Lys Glu Val Val Lys Ser Val Lys
 325 330 335

Lys Ala Val Ile Met Asn Ile Lys Ser Pro Glu His Pro Arg Gly Ser
 340 345 350

Gly Met Ser Val Tyr Tyr Pro Ala Arg Asp Asn His Lys Arg Phe Ala
 355 360 365

Glu Lys Ser Lys Ile Tyr Arg Leu Leu Asp Phe Ser Ser Arg Tyr Gln
 370 375 380

Thr Phe Ile Lys Asp Tyr Ser His Ser Thr Phe Asn Phe Asp Leu
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<210> 151

<211> 1170

<212> DNA

<213> Bacillus licheniformis

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<221> CDS

<222> (501)..(674)

<223>

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 aaaatgaaaa gcgcagaacc gatatacaac gacttgtaaa aacgatagat caaagggaaa 360
 aggcgataac atgccttttc ctttttagca ttcggaataa ttcgccctaa acatttccat 420
 actgaacata tgggcggaac gtccgcgggt aaattgaaaa tgcccggggc cataaatttt 480
 ccgggcagcg gaggaataat atg aaa aca atc gaa cgg tta tta ttt aag ata 533
 Met Lys Thr Ile Glu Arg Leu Leu Phe Lys Ile
 1 5 10
 ctc gtc gta cag acg gtc att tta atc agc gtg cag ctt ctt ttt cat 581
 Leu Val Val Gln Thr Val Ile Leu Ile Ser Val Gln Leu Leu Phe His
 15 20 25
 ttc tcc aag gct gag cct tat ctg tca aag gtc gtg cag tat gaa ggc 629
 Phe Ser Lys Ala Glu Pro Tyr Leu Ser Lys Val Val Gln Tyr Glu Gly
 30 35 40
 gtg aac aac atg aaa atc ggc gaa tgg atc gag aca ttt aag ccg 674

10294.000.ST25.txt

Val Asn Asn Met Lys Ile Gly Glu Trp Ile Glu Thr Phe Lys Pro
45 50 55

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ccagatagca aggagaggaa ttatggaaaa gaaattatgc attgcaatag acggccctgc 794
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cggaaccac gttctc 1170

<210> 152

<211> 58

<212> PRT

<213> Bacillus licheniformis

<400> 152

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Val Ile Leu Ile Ser Val Gln Leu Leu Phe His Phe Ser Lys Ala Glu
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Pro Tyr Leu Ser Lys Val Val Gln Tyr Glu Gly Val Asn Asn Met Lys
35 40 45

Ile Gly Glu Trp Ile Glu Thr Phe Lys Pro
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<210> 153

<211> 1435

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(932)

<223>

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cgtcttcacatc aaaaccggcc agttcatatt tgaagacgga gtattcctcg ccgtcgtcaa 180
atttcgacgt gtcttcctcc ccgtttccag taatgtgaac ataatttcg tccgtcccca 240
cacggtttta gttacatccg cttaaaaatg cggcaaatat gatcatcagg ctgatccatg 300
gaatatgggt ttttcacttt ttctcctcat ttatggtttc tgtgtaaag ataagattca 360
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Met Lys Lys Ile Val Cys Leu Met Val Phe Ser
1 5 10
) atc atg acg gcc ttc ggt att cac atc cag cct gct gaa gct gcg gtt 581
Ile Met Thr Ala Phe Gly Ile His Ile Gln Pro Ala Glu Ala Ala Val
15 20 25
ata aaa gat gag aaa aag atg acc atg aca atg act gaa gat cat gtg 629
Ile Lys Asp Glu Lys Lys Met Thr Met Thr Met Thr Glu Asp His Val
30 35 40
gga ttt ttt atg gcg gac agc acc aat gta aat tac tac ccg aca tgg 677
Gly Phe Phe Met Ala Asp Ser Thr Asn Val Asn Tyr Tyr Pro Thr Trp
45 50 55
ctg tat tac aag ctt acg att ttt aac gcg gaa ggc tgc aca ctc aac 725
Leu Tyr Tyr Lys Leu Thr Ile Phe Asn Ala Glu Gly Cys Thr Leu Asn
60 65 70 75
atc aag ctg cag aga atc acg tta aca gga cat gcg gtc act tta agc 773
Ile Lys Leu Gln Arg Ile Thr Leu Thr Gly His Ala Val Thr Leu Ser
80 85 90
gag aaa gag tat acg gga aat cat ctt cat tta agt gct gca gat aaa 821
Glu Lys Glu Tyr Thr Gly Asn His Leu His Leu Ser Ala Ala Asp Lys
95 100 105
) gtg agc ggg tcg ccg cac cga aat cat ttc ttg gat atc aca aaa gtg 869
Val Ser Gly Ser Pro His Arg Asn His Phe Leu Asp Ile Thr Lys Val
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tcg ggg tgc ggg gat gtt gga atc aca ggt ttt tac ggc ttt gag cac 917
Ser Gly Cys Gly Asp Val Gly Ile Thr Gly Phe Tyr Gly Phe Glu His
125 130 135
caa atg ccg ggc tac taattgatat agaaagcgcg ggaggggact tttccagagt 972
Gln Met Pro Gly Tyr
140
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ttaaattatc gacttttagag ggcggtgaca tcgaactgaa aaaatgacgg ggaaaggcgg 1212
tgcttgatcaa cttttggggg gctttttgta caccgtgcaa agaggagatg cccgtcatgc 1272

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<210> 154

<211> 144

<212> PRT

<213> Bacillus licheniformis

<400> 154

Met Lys Lys Ile Val Cys Leu Met Val Phe Ser Ile Met Thr Ala Phe
1 5 10 15

Gly Ile His Ile Gln Pro Ala Glu Ala Ala Val Ile Lys Asp Glu Lys
20 25 30

Lys Met Thr Met Thr Met Thr Glu Asp His Val Gly Phe Phe Met Ala
35 40 45

Asp Ser Thr Asn Val Asn Tyr Tyr Pro Thr Trp Leu Tyr Tyr Lys Leu
50 55 60

Thr Ile Phe Asn Ala Glu Gly Cys Thr Leu Asn Ile Lys Leu Gln Arg
65 70 75 80

Ile Thr Leu Thr Gly His Ala Val Thr Leu Ser Glu Lys Glu Tyr Thr
85 90 95

Gly Asn His Leu His Leu Ser Ala Ala Asp Lys Val Ser Gly Ser Pro
100 105 110

His Arg Asn His Phe Leu Asp Ile Thr Lys Val Ser Gly Cys Gly Asp
115 120 125

Val Gly Ile Thr Gly Phe Tyr Gly Phe Glu His Gln Met Pro Gly Tyr
130 135 140

<210> 155

<211> 1768

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1265)

<223>

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acggcctatt tggcaggcta catcgctgaa aaatataatt acgatgatga agagcttttt      180
ccgcgggcga aaagcaaaat cagcggctac atcgagtcac atatcgattc caccctgtcc      240
gggtacagct cagtcgatgt gaaaacgaaa cacgtcgata cacaaaaagt gaaaagcttg      300
tatgtgcttt tgcccgtctg gatgggtcaat tacaactaca aacaaaagga ttacatcttt      360
gccatgaacg gacaaacggg aaaagtcgtc ggcaagccgc cgatcagctc atttaaagaa      420
aaaatgtggt tcagcggggct ggccgtctcc atatttgcac tctggaaaat cattgctgct      480
gtaatgggag gcggggcgctg atg aga agt tta ttg aga agc gcg atg atc tta      533
                    Met Arg Ser Leu Leu Arg Ser Ala Met Ile Leu
                    1             5             10

tgt atg att ttc ctt gtc ttc atc cct ata gcc tcc ggt gcg gca gcc      581
Cys Met Ile Phe Leu Val Phe Ile Pro Ile Ala Ser Gly Ala Ala Ala
                    15             20             25

tct gaa cag aag cgg ttt gtt tat gat gaa gcc ggg ctt ctg acc aaa      629
Ser Glu Gln Lys Arg Phe Val Tyr Asp Glu Ala Gly Leu Leu Thr Lys
                    30             35             40

cag gaa atc gag aag ctg gaa acg ctg gca gcc aaa ttg ggc gcc gaa      677
Gln Glu Ile Glu Lys Leu Glu Thr Leu Ala Ala Lys Leu Gly Ala Glu
                    45             50             55

cgg gag acc gac ttt atc att gtg acg acc aat gat aca aac ggc cgc      725
Arg Glu Thr Asp Phe Ile Ile Val Thr Thr Asn Asp Thr Asn Gly Arg
                    60             65             70             75

gat gta aag aaa tat gcg gag gac ttc tat gac gaa aaa gcg ccc ggc      773
Asp Val Lys Lys Tyr Ala Glu Asp Phe Tyr Asp Glu Lys Ala Pro Gly
                    80             85             90

tac cag aag aag cac gga aat gca gcc gta tta acg gta gat atg gag      821
Tyr Gln Lys Lys His Gly Asn Ala Ala Val Leu Thr Val Asp Met Glu
                    95             100             105

cat aga gaa gtc tat ctt gcc ggc ttt aaa aag gct gaa gaa tat ttg      869
His Arg Glu Val Tyr Leu Ala Gly Phe Lys Lys Ala Glu Glu Tyr Leu
                    110             115             120

aat gac gcc agg ctg gac aaa att aga gaa aaa atc acg ccg gat ata      917
Asn Asp Ala Arg Leu Asp Lys Ile Arg Glu Lys Ile Thr Pro Asp Ile
                    125             130             135

tcc gac aag cat tat gag gcc gca ttc gaa atg ttt atg aag gcg gcg      965
Ser Asp Lys His Tyr Glu Ala Ala Phe Glu Met Phe Met Lys Ala Ala
                    140             145             150             155

cat gat gat atg gag aag aaa ccg tgg gcg gac agc atc ttt ttt aag      1013
His Asp Asp Met Glu Lys Lys Pro Trp Ala Asp Ser Ile Phe Phe Lys
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10294.000.ST25.txt

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Thr Trp Phe Gln Leu Leu Val Ser Ala Val Ile Ala Gly Ile Ala Val
175 180 185

gcc att atg aaa tac aat tca ggc ggc aaa gtg aca gta agt gca agc 1109
Ala Ile Met Lys Tyr Asn Ser Gly Gly Lys Val Thr Val Ser Ala Ser
190 195 200

act tat atg aac ggt gat acg tcc gga gtg atc aga aat aat gac gaa 1157
Thr Tyr Met Asn Gly Asp Thr Ser Gly Val Ile Arg Asn Asn Asp Glu
205 210 215

tac atc aga acg acc gtc aca aaa cag aga aaa ccg tcc aat aat aaa 1205
Tyr Ile Arg Thr Thr Val Thr Lys Gln Arg Lys Pro Ser Asn Asn Lys
220 225 230 235

agc tca ggc ggc gga acg acg agc gga ggc cat tcg cac agc ggc agc 1253
Ser Ser Gly Gly Gly Thr Thr Ser Gly Gly His Ser His Ser Gly Ser
240 245 250

cgg gga agc ttt tagaaagggg aaggaagagc ttaaattggtg ttttttagaa 1305
Arg Gly Ser Phe
255

atcaatttgc aaatgtagta gagtgggatg aatttcgcga tgatatgatt ttctataaat 1365
ggaacaaccg cgaaatcaaaa aaggggagcc ggctgatcat tcgccccggt caggatgccg 1425
tcttttttaa caacggaaaa attgaaggca ttttccagga tgagggcgac tatgatattg 1485
aatccgaaat tattcctttt ttatccactt taaaagggtt taaatttggc tttaacagcg 1545
ggatgcgcgc cgaagtcctg tttgtcaaca cgaaggaatt taccgtcaag tgggggacga 1605
agaatgccat caatatcccc gctgcaggac ttccgggcgg catgccgac agggcgaacg 1665
gaagatttaa ctttaagggtg aatgattatg tcgcattaat cgataaaaatt gccggtgtga 1725
aagatcagta tgttgtggaa gatatcaaaa tacggatcac atc 1768

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<210> 156

<211> 255

<212> PRT

<213> Bacillus licheniformis

<400> 156

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Met Arg Ser Leu Leu Arg Ser Ala Met Ile Leu Cys Met Ile Phe Leu
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Val Phe Ile Pro Ile Ala Ser Gly Ala Ala Ala Ser Glu Gln Lys Arg
20 25 30

Phe Val Tyr Asp Glu Ala Gly Leu Leu Thr Lys Gln Glu Ile Glu Lys
35 40 45

Leu Glu Thr Leu Ala Ala Lys Leu Gly Ala Glu Arg Glu Thr Asp Phe
50 55 60

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Ile Ile Val Thr Thr Asn Asp Thr Asn Gly Arg Asp Val Lys Lys Tyr
65          70          75          80

Ala Glu Asp Phe Tyr Asp Glu Lys Ala Pro Gly Tyr Gln Lys Lys His
85          90          95

Gly Asn Ala Ala Val Leu Thr Val Asp Met Glu His Arg Glu Val Tyr
100         105         110

Leu Ala Gly Phe Lys Lys Ala Glu Glu Tyr Leu Asn Asp Ala Arg Leu
115         120         125

Asp Lys Ile Arg Glu Lys Ile Thr Pro Asp Ile Ser Asp Lys His Tyr
130         135         140

Glu Ala Ala Phe Glu Met Phe Met Lys Ala Ala His Asp Asp Met Glu
145         150         155         160

Lys Lys Pro Trp Ala Asp Ser Ile Phe Phe Lys Thr Trp Phe Gln Leu
165         170         175

Leu Val Ser Ala Val Ile Ala Gly Ile Ala Val Ala Ile Met Lys Tyr
180         185         190

Asn Ser Gly Gly Lys Val Thr Val Ser Ala Ser Thr Tyr Met Asn Gly
195         200         205

Asp Thr Ser Gly Val Ile Arg Asn Asn Asp Glu Tyr Ile Arg Thr Thr
210         215         220

Val Thr Lys Gln Arg Lys Pro Ser Asn Asn Lys Ser Ser Gly Gly Gly
225         230         235         240

Thr Thr Ser Gly Gly His Ser His Ser Gly Ser Arg Gly Ser Phe
245         250         255

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<210> 157

<211> 1688

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1652)

<223>

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cgaatcaggc	tgacgcagga	tcctttttcag	gaggctgcag	ccgaaaggac	gctctatcag											120		
gtctatcatc	gatgcataga	agaatttttt	acaccgaaaa	aagatacttg	gtacgaagac											180		
agcagagcgg	cctacacggg	aaaaaacgcc	atttgctttc	acgaaccagc	gccggcctca											240		
ttaaaaaatt	tgatggcttc	gcttgaaaca	ggatatcaat	cgatgagaga	agaattggaa											300		
tactatgcga	ctgactatcg	aatgaagatg	gttcagccga	gatcatagct	taaatgaacc											360		
gtgagccgga	actccccctt	tcataaaagg	gggggttttta	tcttgcttta	gattttttctc											420		
gggaaatcat	ccaattggtg	ttcataacaa	aaagacaagc	gcataaactt	gtacaaacaa											480		
ccacaaggac	gtgagaaaaa	atg cgc ttt ttt cta aaa caa gcg gca gca gcc											533					
		Met Arg Phe Phe	Leu Lys Gln Ala Ala Ala															
		1	5	10														
atc atg ata tgc tct ctt tta tgc tct tca tac gaa acc gct caa gca											581							
Ile Met Ile Cys Ser Leu Leu Cys Ser Ser Tyr Glu Thr Ala Gln Ala																		
		15	20	25														
cag ccc tcc ctt cat atc agc gca aaa agc gcg att gtc atg gac ggg											629							
Gln Pro Ser Leu His Ile Ser Ala Lys Ser Ala Ile Val Met Asp Gly																		
		30	35	40														
caa tcc gga cgg gtt ttg ttt gca aag gat gag cat gaa aaa cgg cgc											677							
Gln Ser Gly Arg Val Leu Phe Ala Lys Asp Glu His Glu Lys Arg Arg																		
		45	50	55														
att gca agc att acg aag att atg aca gcc att ttg gcc gtg gaa tcg											725							
Ile Ala Ser Ile Thr Lys Ile Met Thr Ala Ile Leu Ala Val Glu Ser																		
		60	65	70	75													
ggc aaa ttg gat gag acg gtc acg gtc agc gac aga gcg gtc agg aca											773							
Gly Lys Leu Asp Glu Thr Val Thr Val Ser Asp Arg Ala Val Arg Thr																		
		80	85	90														
gag gga tca tcg atc tat tta aca agc ggg caa aag gtg aag ctg aag											821							
Glu Gly Ser Ser Ile Tyr Leu Thr Ser Gly Gln Lys Val Lys Leu Lys																		
		95	100	105														
gac ctt gtt tac ggt ttg atg ctg aga tcg gga aat gat gca gcc gtt											869							
Asp Leu Val Tyr Gly Leu Met Leu Arg Ser Gly Asn Asp Ala Ala Val																		
		110	115	120														
gcg att gcc gaa cat gtg ggc gga agc ctg gaa ggc ttt gtc tac atg											917							
Ala Ile Ala Glu His Val Gly Gly Ser Leu Glu Gly Phe Val Tyr Met																		
		125	130	135														
atg aat caa aaa gcg gcc gag ctc ggc atg gaa aac acc ctg ttc cgc											965							
Met Asn Gln Lys Ala Ala Glu Leu Gly Met Glu Asn Thr Leu Phe Arg																		
		140	145	150	155													
aat ccg cac gga ctt gat gac cac cct gat cac tat tcc tcg gcc tat											1013							
Asn Pro His Gly Leu Asp Asp His Pro Asp His Tyr Ser Ser Ala Tyr																		
		160	165	170														
gat atg gcg ctt tta aca aaa tat gcg atg agc aat gaa acg tac aaa											1061							
Asp Met Ala Leu Leu Thr Lys Tyr Ala Met Ser Asn Glu Thr Tyr Lys																		
		175	180	185														
aaa atc gcc gga acg aaa cgc tat aaa gca gaa acg atg caa ggc atc											1109							

10294.000.ST25.txt

Lys Ile Ala Gly Thr Lys Arg Tyr Lys Ala Glu Thr Met Gln Gly Ile
 190 195 200
 tgg gag aat aaa aac aag ctt tta aca ggg ctt tac aaa tac agt aca 1157
 Trp Glu Asn Lys Asn Lys Leu Leu Thr Gly Leu Tyr Lys Tyr Ser Thr
 205 210 215
 ggc ggg aag acg gga tat aca agg ctt gca aag cgg acg ctc gtc tcc 1205
 Gly Gly Lys Thr Gly Tyr Thr Arg Leu Ala Lys Arg Thr Leu Val Ser
 220 225 230 235
 att tca tcg aaa gac gga acc gat ttg atc gcc gtc aca atc aat gcc 1253
 Ile Ser Ser Lys Asp Gly Thr Asp Leu Ile Ala Val Thr Ile Asn Ala
 240 245 250
 cct gac gac tgg aat gat cat atg aac atg ttc aac tat gta ttc ggc 1301
 Pro Asp Asp Trp Asn Asp His Met Asn Met Phe Asn Tyr Val Phe Gly
 255 260 265
 cag tac aaa aca tat atc atc gcc aaa aaa ggc gag att ccg aaa tta 1349
 Gln Tyr Lys Thr Tyr Ile Ile Ala Lys Lys Gly Glu Ile Pro Lys Leu
 270 275 280
 aaa gac tct ttt tac gga cat aca gct ttt att aaa cgg gat gtc aca 1397
 Lys Asp Ser Phe Tyr Gly His Thr Ala Phe Ile Lys Arg Asp Val Thr
 285 290 295
 tat ctt tta aac gaa gag gaa aaa gaa gat gtg aag gtt gat atc gag 1445
 Tyr Leu Leu Asn Glu Glu Glu Lys Glu Asp Val Lys Val Asp Ile Glu
 300 305 310 315
 ctt ctt gaa ccg aaa aaa tca tgg cgt aaa aac aaa aaa gaa atc ccg 1493
 Leu Leu Glu Pro Lys Lys Ser Trp Arg Lys Asn Lys Lys Glu Ile Pro
 320 325 330
 gac atc atc gga gaa atg aac gtc atg ttc gac gga aaa acg att gca 1541
 Asp Ile Ile Gly Glu Met Asn Val Met Phe Asp Gly Lys Thr Ile Ala
 335 340 345
 agc gta ccg atc tat tat gaa aac gag cga aac aaa aat ccg aaa aaa 1589
 Ser Val Pro Ile Tyr Tyr Glu Asn Glu Arg Asn Lys Asn Pro Lys Lys
 350 355 360
 tcg ttt ttc gag acc ttt caa tcc gta ttc caa aaa gcg gcg ggc ggt 1637
 Ser Phe Phe Glu Thr Phe Gln Ser Val Phe Gln Lys Ala Ala Gly Gly
 365 370 375
 tca tca tgg tca ata taatctgggt cggcttaacg gtgatcggta tgggtgt 1688
 Ser Ser Trp Ser Ile
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<210> 158

<211> 384

<212> PRT

<213> Bacillus licheniformis

<400> 158

Met Arg Phe Phe Leu Lys Gln Ala Ala Ala Ala Ile Met Ile Cys Ser
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10294.000.ST25.txt

Leu Leu Cys Ser Ser Tyr Glu Thr Ala Gln Ala Gln Pro Ser Leu His
 20 25 30
 Ile Ser Ala Lys Ser Ala Ile Val Met Asp Gly Gln Ser Gly Arg Val
 35 40 45
 Leu Phe Ala Lys Asp Glu His Glu Lys Arg Arg Ile Ala Ser Ile Thr
 50 55 60
 Lys Ile Met Thr Ala Ile Leu Ala Val Glu Ser Gly Lys Leu Asp Glu
 65 70 75 80
 Thr Val Thr Val Ser Asp Arg Ala Val Arg Thr Glu Gly Ser Ser Ile
 85 90 95
 Tyr Leu Thr Ser Gly Gln Lys Val Lys Leu Lys Asp Leu Val Tyr Gly
 100 105 110
 Leu Met Leu Arg Ser Gly Asn Asp Ala Ala Val Ala Ile Ala Glu His
 115 120 125
 Val Gly Gly Ser Leu Glu Gly Phe Val Tyr Met Met Asn Gln Lys Ala
 130 135 140
 Ala Glu Leu Gly Met Glu Asn Thr Leu Phe Arg Asn Pro His Gly Leu
 145 150 155 160
 Asp Asp His Pro Asp His Tyr Ser Ser Ala Tyr Asp Met Ala Leu Leu
 165 170 175
 Thr Lys Tyr Ala Met Ser Asn Glu Thr Tyr Lys Lys Ile Ala Gly Thr
 180 185 190
 Lys Arg Tyr Lys Ala Glu Thr Met Gln Gly Ile Trp Glu Asn Lys Asn
 195 200 205
 Lys Leu Leu Thr Gly Leu Tyr Lys Tyr Ser Thr Gly Gly Lys Thr Gly
 210 215 220
 Tyr Thr Arg Leu Ala Lys Arg Thr Leu Val Ser Ile Ser Ser Lys Asp
 225 230 235 240
 Gly Thr Asp Leu Ile Ala Val Thr Ile Asn Ala Pro Asp Asp Trp Asn
 245 250 255
 Asp His Met Asn Met Phe Asn Tyr Val Phe Gly Gln Tyr Lys Thr Tyr
 260 265 270
 Ile Ile Ala Lys Lys Gly Glu Ile Pro Lys Leu Lys Asp Ser Phe Tyr
 275 280 285

Gly His Thr Ala Phe Ile Lys Arg Asp Val Thr Tyr Leu Leu Asn Glu
 290 295 300

Glu Glu Lys Glu Asp Val Lys Val Asp Ile Glu Leu Leu Glu Pro Lys
 305 310 315 320

Lys Ser Trp Arg Lys Asn Lys Lys Glu Ile Pro Asp Ile Ile Gly Glu
 325 330 335

Met Asn Val Met Phe Asp Gly Lys Thr Ile Ala Ser Val Pro Ile Tyr
 340 345 350

Tyr Glu Asn Glu Arg Asn Lys Asn Pro Lys Lys Ser Phe Phe Glu Thr
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<210> 159

<211> 1617

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1118)

<223>

<400> 159
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 aattcagcgg gtgaggtggt cgacatgagg aaaggagtag tccttggttct gttcgctatg 180
 ctgttattgg caggctgcgg cacaacgcag cataatgggc aaagcgggtga tgagagccga 240
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 cataccgtcg ccgtcaatat tgacggcaaa gaaacgatgt ttcagggtccc tcccgaaaaa 360
 cgggacaaat ataaagggat cgaggatgat acaaaggtag aagtggagta cacgaaagca 420
 gaggacggaa cattacagct tgaagatatg aaaaagaaag aatgatcggt tgcaaaaagg 480
 gattgtagga ggaacaaatc gtg aaa ctg tta ata aag agt ttt gtt ttg ctg 533
 Val Lys Leu Leu Ile Lys Ser Phe Val Leu Leu
 1 5 10
 ctg ttt tcg ttt atg gcg gct ttt cca gct gct ttt gcg gct gag ccg 581
 Leu Phe Ser Phe Met Ala Ala Phe Pro Ala Ala Phe Ala Ala Glu Pro
 15 20 25

10294.000.ST25.txt

ctt tcc ggg aag acg gta tat gtt gac gca ggt cac ggg ggt gaa gac Leu Ser Gly Lys Thr Val Tyr Val Asp Ala Gly His Gly Glu Asp 30 35 40	629
agc ggt gct gtc gga aac ggg ctg ctt gag aaa gat gtc aac ctt gaa Ser Gly Ala Val Gly Asn Gly Leu Leu Glu Lys Asp Val Asn Leu Glu 45 50 55	677
gtg gca atg ctg att gat gaa aag ctg aaa gaa gaa gga gcc gac aca Val Ala Met Leu Ile Asp Glu Lys Leu Lys Glu Glu Gly Ala Asp Thr 60 65 70 75	725
gtc gcc tca aga acg gat gat acg ttt ttg acg ctg gaa gac cgg gtg Val Ala Ser Arg Thr Asp Asp Thr Phe Leu Thr Leu Glu Asp Arg Val 80 85 90	773
gcc aag gcg agc aaa aat gct tca gac ttg ttt atc agc att cat gca Ala Lys Ala Ser Lys Asn Ala Ser Asp Leu Phe Ile Ser Ile His Ala 95 100 105	821
aac tcg gcc gtc cct gaa gcg tcc ggt aca gaa aca tat ttc gat tcc Asn Ser Ala Val Pro Glu Ala Ser Gly Thr Glu Thr Tyr Phe Asp Ser 110 115 120	869
acg tat caa gcc gct gac agc gaa cgg ctg gca tct gac att caa gag Thr Tyr Gln Ala Ala Asp Ser Glu Arg Leu Ala Ser Asp Ile Gln Glu 125 130 135	917
cgg ctt ccg gat gcg ctg ggc act cgg gac aga ggt gta aaa gaa tca Arg Leu Pro Asp Ala Leu Gly Thr Arg Asp Arg Gly Val Lys Glu Ser 140 145 150 155	965
ggg ttt tat gtc atc aaa aat tct caa atg ccg agt gtt tta gtc gaa Gly Phe Tyr Val Ile Lys Asn Ser Gln Met Pro Ser Val Leu Val Glu 160 165 170	1013
ctg ggc ttt atc aca aac aaa act gat gca gat aaa ctc gaa agt ccg Leu Gly Phe Ile Thr Asn Lys Thr Asp Ala Asp Lys Leu Glu Ser Pro 175 180 185	1061
gaa tat cag gaa aaa gct gca gac gcg att gct gac gct gtc gta tct Glu Tyr Gln Glu Lys Ala Ala Asp Ala Ile Ala Asp Ala Val Val Ser 190 195 200	1109
tat tat gaa taatagaagg gccctggtat atgaccgggg ttcttgtgtt Tyr Tyr Glu 205	1158
atgtttatgt taaaaaaggc cttatgtgtg gaaagaaaac agtaagacct tcataatggg	1218
ttataaactt gcaattcttg tagagggtgaa ccagaaatga cgaaaatatt tgcacacaga	1278
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catgatgaaa agcttgacag gacgacttca ctgaaaggggt atgtgaaaga tcttacatat	1458
gaggaaataa aacatggaga cgcaagccac cgttttgccg aaaaaaccgg ttctgtccct	1518
gtgccgaccc ttgaagaagt gtttgagtgg gcggcagatg ctgaatttct tcttaatgtt	1578
gaattgaaaa acagcattat ccgctatgaa gggatggaa	1617

<210> 160

<211> 206

<212> PRT

<213> Bacillus licheniformis

<400> 160

Val Lys Leu Leu Ile Lys Ser Phe Val Leu Leu Leu Phe Ser Phe Met
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 20 25 30

Val Tyr Val Asp Ala Gly His Gly Gly Glu Asp Ser Gly Ala Val Gly
 35 40 45

Asn Gly Leu Leu Glu Lys Asp Val Asn Leu Glu Val Ala Met Leu Ile
 50 55 60

Asp Glu Lys Leu Lys Glu Glu Gly Ala Asp Thr Val Ala Ser Arg Thr
 65 70 75 80

Asp Asp Thr Phe Leu Thr Leu Glu Asp Arg Val Ala Lys Ala Ser Lys
 85 90 95

Asn Ala Ser Asp Leu Phe Ile Ser Ile His Ala Asn Ser Ala Val Pro
 100 105 110

Glu Ala Ser Gly Thr Glu Thr Tyr Phe Asp Ser Thr Tyr Gln Ala Ala
 115 120 125

Asp Ser Glu Arg Leu Ala Ser Asp Ile Gln Glu Arg Leu Pro Asp Ala
 130 135 140

Leu Gly Thr Arg Asp Arg Gly Val Lys Glu Ser Gly Phe Tyr Val Ile
 145 150 155 160

Lys Asn Ser Gln Met Pro Ser Val Leu Val Glu Leu Gly Phe Ile Thr
 165 170 175

Asn Lys Thr Asp Ala Asp Lys Leu Glu Ser Pro Glu Tyr Gln Glu Lys
 180 185 190

Ala Ala Asp Ala Ile Ala Asp Ala Val Val Ser Tyr Tyr Glu
 195 200 205

<210> 161

<211> 1803

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (165)..(1487)

<223>

<400> 161

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cattcctcct tgagagcgtt ttcttaacaa acgggaggga tcgt atg aaa aag tta 176
Met Lys Lys Leu
1tgt tgc ctg atc ttg gtc ttg gtt ttt tcc gcg ggc tgt act cag caa 224
Cys Cys Leu Ile Leu Val Leu Val Phe Ser Ala Gly Cys Thr Gln Gln
5 10 15 20aag gca tca acg gaa gag gac ggg gcg ctt gaa atc aat tgg ctc gta 272
Lys Ala Ser Thr Glu Glu Asp Gly Ala Leu Glu Ile Asn Trp Leu Val
25 30 35ccg ctc cac aca ccg cag cct ccg aaa gag aag gcg ctt gac atc att 320
Pro Leu His Thr Pro Gln Pro Pro Lys Glu Lys Ala Leu Asp Ile Ile
40 45 50gaa gac aaa acg aat aca aag ctg aag ctc atc tgg gtt ccg gat tca 368
Glu Asp Lys Thr Asn Thr Lys Leu Lys Leu Ile Trp Val Pro Asp Ser
55 60 65aca aaa gaa gag cgg atc aat aca acc ctt gca agc gga aac atg cct 416
Thr Lys Glu Glu Arg Ile Asn Thr Thr Leu Ala Ser Gly Asn Met Pro
70 75 80aaa gta atg aca ttg cct gat ctt gaa gat tca gcg gtt gtc agc gcg 464
Lys Val Met Thr Leu Pro Asp Leu Glu Asp Ser Ala Val Val Ser Ala
85 90 95 100ctg cgc tcg gga atg ttc tgg gaa atc gga ccg tat ttc aaa gac tat 512
Leu Arg Ser Gly Met Phe Trp Glu Ile Gly Pro Tyr Phe Lys Asp Tyr
105 110 115ccg aat tta aga aaa ctt gat aaa act ata ttg aaa aat att tcg gtt 560
Pro Asn Leu Arg Lys Leu Asp Lys Thr Ile Leu Lys Asn Ile Ser Val
120 125 130gat ggc aaa gtt tac ggg att tat aga gaa agg ccg atg gcc agg cag 608
Asp Gly Lys Val Tyr Gly Ile Tyr Arg Glu Arg Pro Met Ala Arg Gln
135 140 145gga gtc gtg att cgg aaa gac tgg ctc gac aat ctc gga ttg gaa atg 656
Gly Val Val Ile Arg Lys Asp Trp Leu Asp Asn Leu Gly Leu Glu Met
150 155 160ccg gaa acc gtt gat gac ctt tat aaa ata gcg aaa gca ttt aca gaa 704
Pro Glu Thr Val Asp Asp Leu Tyr Lys Ile Ala Lys Ala Phe Thr Glu
165 170 175 180

cag gac ccc gat caa aac gga aaa gac gac acg ttc ggt ctc gcc gac 752

10294.000.ST25.txt

Gln	Asp	Pro	Asp	Gln 185	Asn	Gly	Lys	Asp	Asp 190	Thr	Phe	Gly	Leu	Ala 195	Asp	
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Arg	Asn	Asp	Leu 200	Thr	Phe	Gly	Ala	Phe 205	Lys	Thr	Leu	Ala	Ser 210	Tyr	Phe	
ggc	gcg	ccg	aac	gaa	tgg	gga	acg	gac	gaa	gac	gga	aat	ctc	ttc	ccc	848
Gly	Ala	Pro 215	Asn	Glu	Trp	Gly	Thr 220	Asp	Glu	Asp	Gly	Asn 225	Leu	Phe	Pro	
tat	ttt	aag	cat	gag	gcc	tat	aaa	gac	gca	atg	gca	tac	atg	aaa	aag	896
Tyr	Phe 230	Lys	His	Glu	Ala	Tyr 235	Lys	Asp	Ala	Met	Ala 240	Tyr	Met	Lys	Lys	
ctt	tat	gaa	gaa	ggc	ctg	atg	aac	agg	gac	ttt	gcg	gtg	aca	agc	aaa	944
Leu 245	Tyr	Glu	Glu	Gly	Leu 250	Met	Asn	Arg	Asp	Phe 255	Ala	Val	Thr	Ser	Lys 260	
acg	cag	cag	cag	gat	tta	gtg	att	cag	ggg	aaa	gcg	gga	atc	tat	atc	992
Thr	Gln	Gln	Gln	Asp 265	Leu	Val	Ile	Gln	Gly 270	Lys	Ala	Gly	Ile	Tyr 275	Ile	
ggc	gcg	atg	agc	gat	gcc	atg	aac	ttg	cgt	gat	cag	gga	ctc	gct	ttg	1040
Gly	Ala	Met	Ser 280	Asp	Ala	Met	Asn	Leu 285	Arg	Asp	Gln	Gly	Leu 290	Ala	Leu	
aac	ccc	ggc	ttt	cag	ctt	gat	atc	gca	aac	cgg	atc	aag	ggc	ccc	gac	1088
Asn	Pro	Gly 295	Phe	Gln	Leu	Asp	Ile 300	Ala	Asn	Arg	Ile	Lys 305	Gly	Pro	Asp	
ggc	aag	gag	cg	aca	tgg	gcg	ctc	ggc	ggg	cat	ggc	ggg	atg	ttc	gcc	1136
Gly	Lys 310	Glu	Arg	Thr	Trp	Ala 315	Leu	Gly	Gly	His	Gly 320	Gly	Met	Phe	Ala	
att	tcg	aaa	tca	agc	gtc	aag	act	gaa	aaa	gag	gtc	aga	aaa	atc	ctc	1184
Ile 325	Ser	Lys	Ser	Ser	Val 330	Lys	Thr	Glu	Lys	Glu 335	Val	Arg	Lys	Ile	Leu 340	
gca	ttt	ttt	gac	aga	atc	gct	gaa	gaa	gac	ctc	aac	aat	ttg	atg	ttg	1232
Ala	Phe	Phe	Asp	Arg 345	Ile	Ala	Glu	Glu	Asp 350	Leu	Asn	Asn	Leu	Met 355	Leu	
tat	gga	ata	gaa	ggc	gta	cac	tat	gaa	aag	aaa	ggg	ggg	agc	ggc	tat	1280
Tyr	Gly	Ile	Glu 360	Gly	Val	His	Tyr	Glu 365	Lys	Lys	Gly	Gly	Ser 370	Gly	Tyr	
ttt	cga	aag	cag	gaa	aac	tac	cat	ctg	tgg	gaa	gcg	gaa	att	cag	ccg	1328
Phe	Arg	Lys 375	Gln	Glu	Asn	Tyr	His 380	Leu	Trp	Glu	Ala	Glu 385	Ile	Gln	Pro	
tta	aac	cag	ctg	att	ggc	gtc	aat	aaa	caa	gct	tta	aaa	agc	gct	gaa	1376
Leu	Asn 390	Gln	Leu	Ile	Gly	Val 395	Asn	Lys	Gln	Ala	Leu 400	Lys	Ser	Ala	Glu	
gat	ccg	ctc	cg	gcc	aaa	aat	gaa	aag	ctt	gag	gag	gac	aac	cgg	gca	1424
Asp 405	Pro	Leu	Arg	Ala 410	Lys	Asn	Glu	Lys	Leu	Glu 415	Glu	Asp	Asn	Arg	Ala 420	
atc	gca	gtc	cag	aat	ccg	gcc	gaa	ccg	tgt	att	ctg	ccg	cac	aga	tgg	1472
Ile	Ala	Val	Gln	Asn 425	Pro	Ala	Glu	Pro	Cys 430	Ile	Leu	Pro	His	Arg 435	Trp	
aca	ggg	gaa	cag	aat	tga	a	a	a	a	a	a	a	a	a	a	1527
Thr	Gly	Glu	Gln 440	Asn												
cg	g	g	a	a	a	a	a	a	a	a	a	a	a	a	a	1587

10294.000.ST25.txt

ggaaagatca tgaaagaact gaatgaagat ctgaaaaaag caaactaaac agaaaaccct 1647
 ttccattttt ttgaaaagga aagggttttt catcgtattc gctccaagtt cattttcttt 1707
 aaattctgca aaataaaca tataattcca tcataggacg aaaaggagga agcgatatgc 1767
 agactgccgt tatatatgca cacccaaadc caaaca 1803

<210> 162

<211> 441

<212> PRT

<213> *Bacillus licheniformis*

<400> 162

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Cys Thr Gln Gln Lys Ala Ser Thr Glu Glu Asp Gly Ala Leu Glu Ile
 20 25 30

Asn Trp Leu Val Pro Leu His Thr Pro Gln Pro Pro Lys Glu Lys Ala
 35 40 45

Leu Asp Ile Ile Glu Asp Lys Thr Asn Thr Lys Leu Lys Leu Ile Trp
 50 55 60

Val Pro Asp Ser Thr Lys Glu Glu Arg Ile Asn Thr Thr Leu Ala Ser
 65 70 75 80

Gly Asn Met Pro Lys Val Met Thr Leu Pro Asp Leu Glu Asp Ser Ala
 85 90 95

Val Val Ser Ala Leu Arg Ser Gly Met Phe Trp Glu Ile Gly Pro Tyr
 100 105 110

Phe Lys Asp Tyr Pro Asn Leu Arg Lys Leu Asp Lys Thr Ile Leu Lys
 115 120 125

Asn Ile Ser Val Asp Gly Lys Val Tyr Gly Ile Tyr Arg Glu Arg Pro
 130 135 140

Met Ala Arg Gln Gly Val Val Ile Arg Lys Asp Trp Leu Asp Asn Leu
 145 150 155 160

Gly Leu Glu Met Pro Glu Thr Val Asp Asp Leu Tyr Lys Ile Ala Lys
 165 170 175

Ala Phe Thr Glu Gln Asp Pro Asp Gln Asn Gly Lys Asp Asp Thr Phe
 180 185 190

Gly Leu Ala Asp Arg Asn Asp Leu Thr Phe Gly Ala Phe Lys Thr Leu
 195 200 205
 Ala Ser Tyr Phe Gly Ala Pro Asn Glu Trp Gly Thr Asp Glu Asp Gly
 210 215 220
 Asn Leu Phe Pro Tyr Phe Lys His Glu Ala Tyr Lys Asp Ala Met Ala
 225 230 235 240
 Tyr Met Lys Lys Leu Tyr Glu Glu Gly Leu Met Asn Arg Asp Phe Ala
 245 250 255
 Val Thr Ser Lys Thr Gln Gln Gln Asp Leu Val Ile Gln Gly Lys Ala
 260 265 270
 Gly Ile Tyr Ile Gly Ala Met Ser Asp Ala Met Asn Leu Arg Asp Gln
 275 280 285
 Gly Leu Ala Leu Asn Pro Gly Phe Gln Leu Asp Ile Ala Asn Arg Ile
 290 295 300
 Lys Gly Pro Asp Gly Lys Glu Arg Thr Trp Ala Leu Gly Gly His Gly
 305 310 315 320
 Gly Met Phe Ala Ile Ser Lys Ser Ser Val Lys Thr Glu Lys Glu Val
 325 330 335
 Arg Lys Ile Leu Ala Phe Phe Asp Arg Ile Ala Glu Glu Asp Leu Asn
 340 345 350
 Asn Leu Met Leu Tyr Gly Ile Glu Gly Val His Tyr Glu Lys Lys Gly
 355 360 365
 Gly Ser Gly Tyr Phe Arg Lys Gln Glu Asn Tyr His Leu Trp Glu Ala
 370 375 380
 Glu Ile Gln Pro Leu Asn Gln Leu Ile Gly Val Asn Lys Gln Ala Leu
 385 390 395 400
 Lys Ser Ala Glu Asp Pro Leu Arg Ala Lys Asn Glu Lys Leu Glu Glu
 405 410 415
 Asp Asn Arg Ala Ile Ala Val Gln Asn Pro Ala Glu Pro Cys Ile Leu
 420 425 430
 Pro His Arg Trp Thr Gly Glu Gln Asn
 435 440

<210> 163

<211> 1400

<212> DNA

<213> *Bacillus licheniformis*

<220>

<221> CDS

<222> (501)..(983)

<223>

<400> 163

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cgagcaagac taaattttctc attggttaatt cccctttttcc cctcagatta agaaactcac	120
cttttacact gcaaaaaaaaa aaaactatgt aaaaaccata tagaattata tctaatttga	180
tgtgaaatca caatattttct cgaggaaaata acatacacta acgcctagaa tcgataatta	240
gtaaaactct ttaaagtatt aatatgttac aaaagcttta ttctccagcc ttaaactttg	300
actaatgaaa cgcatttagg gtacgataaa aagtcgatgt gaggtgagat aaggtgtcaa	360
ggcgcttttg aaattgaagc atctgctgga taaagtgggtg caatagcatg taagctgccg	420
gcatgaaacc ggcagcattt tttaagcgctc cgacgggaag tctttttttg attaaatttc	480
atgggttagcg agtgaaaaat atg tca aca ata tta tgg ctt gtg agc ttc acg	533
Met Ser Thr Ile Leu Trp Leu Val Ser Phe Thr	
1 5 10	
ctc cac ggt ata ttg att tat ttc gtc atc att ttg aat acg agg ctc	581
Leu His Gly Ile Leu Ile Tyr Phe Val Ile Ile Leu Asn Thr Arg Leu	
15 20 25	
agc gct ttc aag gca gcg gag aaa gag caa aaa cag ctt ttg gaa gaa	629
Ser Ala Phe Lys Ala Ala Glu Lys Glu Gln Lys Gln Leu Leu Glu Glu	
30 35 40	
acc gag aat aca ttg acc gct ttt ttg atg gag tta aaa gac gaa aat	677
Thr Glu Asn Thr Leu Thr Ala Phe Leu Met Glu Leu Lys Asp Glu Asn	
45 50 55	
gaa aaa ctc gtt caa gag att cgg gcg aat gcc gaa aaa gag ccg caa	725
Glu Lys Leu Val Gln Glu Ile Arg Ala Asn Ala Glu Lys Glu Pro Gln	
60 65 70 75	
aga ccg gaa aca cag cct gaa att ccc gct caa acc ccc gtc ctt ccg	773
Arg Pro Glu Thr Gln Pro Glu Ile Pro Ala Gln Thr Pro Val Leu Pro	
80 85 90	
gaa gcg gac gaa tcg cgc gat ctg ccg ctt cac atc gaa gcg atg atc	821
Glu Ala Asp Glu Ser Arg Asp Leu Pro Leu His Ile Glu Ala Met Ile	
95 100 105	
aat gag gtg gag cag gaa gag gat gag ctc aat caa aag gag cag gaa	869
Asn Glu Val Glu Gln Glu Glu Asp Glu Leu Asn Gln Lys Glu Gln Glu	
110 115 120	
gca tcc ata tcc tat gaa gaa gaa gct ctc gca tta gaa aaa cat ggg	917

10294.000.ST25.txt

Ala	Ser	Ile	Ser	Tyr	Glu	Glu	Glu	Ala	Leu	Ala	Leu	Glu	Lys	His	Gly		
125						130				135							
gac	tgg	ggg	aaa	gaa	ttt	ttt	cat	aaa	aca	ggc	ccc	aaa	atg	ggg	ggg		965
Asp	Trp	Gly	Lys	Glu	Phe	Phe	His	Lys	Thr	Gly	Pro	Lys	Met	Gly	Gly		
140					145					150					155		
ggt	ggt	gtt	cca	gtc	tct	taaagaaaaa	aaaaattcaa	cctctcttct									1013
Gly	Gly	Val	Pro	Val	Ser												
				160													
ttggggaggg	ggggggggga	aaaaataagg	tggttgtaga	gggggggagga	atTTTTTTTT												1073
aaaggaaacc	ctcatgggga	gggagatgtg	ctttaaacga	gggagggagc	gaggaaatgg												1133
cactggttcc	ataggatgaa	acgcgcggga	ttgtctccag	aaaacaggga	gaccccggaa												1193
aaggagcggg	gcagccaatt	catcactttt	taagtttcaa	agcctcagca	aatttggggg												1253
ttaaaaattc	acacggaatt	ggttgggagg	gaataaggag	agtttaaaaa	cccgccaatt												1313
tatcaagagg	gagccgcagg	gaggaaaata	caatccacgg	atcctaagtg	gtgagatgtc												1373
atggggggat	atggtttcgg	actcgaa															1400

<210> 164

<211> 161

<212> PRT

<213> Bacillus licheniformis

<400> 164

Met	Ser	Thr	Ile	Leu	Trp	Leu	Val	Ser	Phe	Thr	Leu	His	Gly	Ile	Leu		
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			20					25					30				
Ala	Glu	Lys	Glu	Gln	Lys	Gln	Leu	Leu	Glu	Glu	Thr	Glu	Asn	Thr	Leu		
		35					40					45					
Thr	Ala	Phe	Leu	Met	Glu	Leu	Lys	Asp	Glu	Asn	Glu	Lys	Leu	Val	Gln		
	50					55					60						
Glu	Ile	Arg	Ala	Asn	Ala	Glu	Lys	Glu	Pro	Gln	Arg	Pro	Glu	Thr	Gln		
65				70					75						80		
Pro	Glu	Ile	Pro	Ala	Gln	Thr	Pro	Val	Leu	Pro	Glu	Ala	Asp	Glu	Ser		
				85					90					95			
Arg	Asp	Leu	Pro	Leu	His	Ile	Glu	Ala	Met	Ile	Asn	Glu	Val	Glu	Gln		
			100					105					110				
Glu	Glu	Asp	Glu	Leu	Asn	Gln	Lys	Glu	Gln	Glu	Ala	Ser	Ile	Ser	Tyr		
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10294.000.ST25.txt

Glu Glu Glu Ala Leu Ala Leu Glu Lys His Gly Asp Trp Gly Lys Glu
130 135 140

Phe Phe His Lys Thr Gly Pro Lys Met Gly Gly Gly Gly Val Pro Val
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Ser

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<211> 2644

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (502)..(2142)

<223>

<400> 165
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gaccgccggc ttatttcaca atggattgga caaaagcagc agattcggtt cggaagctgg 180
caggattaaa accggctgca ttattgacgg gacacggtgt accgatgaaa ggaagcgatt 240
tttccgaagc gctccttgat ctatcagacc gcttgcccgc ctctgattcg taaattgtca 300
tatgctgcgc ttaaaacatt cagccaggct gaatgttttt ttatagggaa aaactaacca 360
ttttacatgt gatgatggcc gtccattggt cttaaattccg gatgttgatg tataccaaag 420
gaatcatttt ctgaaatttt agacaaaata tgttgatatt tcatttataa tgcaggtatg 480
cctgaaagga gctgagaaaa g atg aaa att caa aaa agg gtc caa gct ttg 531
Met Lys Ile Gln Lys Arg Val Gln Ala Leu
1 5 10
ctg gca act tcg gca atg ttt gca gga ctg atg ctg tcc gat gcg gtg 579
Leu Ala Thr Ser Ala Met Phe Ala Gly Leu Met Leu Ser Asp Ala Val
15 20 25
tac gct gcg gaa acc cct tac tat gga aag aac tat act cag cca gag 627
Tyr Ala Ala Glu Thr Pro Tyr Tyr Gly Lys Asn Tyr Thr Gln Pro Glu
30 35 40
caa gtg tca tca tta tat ccg gag cct gaa gaa aca ttc tca acc cct 675
Gln Val Ser Ser Leu Tyr Pro Glu Pro Glu Glu Thr Phe Ser Thr Pro
45 50 55
gct ttt gta aaa gaa ggg gaa gcc ttt acg aca caa gaa gaa atg atg 723

10294.000.ST25.txt

Ala	Phe	Val	Lys	Glu	Gly	Glu	Ala	Phe	Thr	Thr	Gln	Glu	Glu	Met	Met	
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aag	ttt	ata	acc	agt	ctg	aca	aag	aaa	agc	ccg	aat	gtc	aaa	atc	ggg	771
Lys	Phe	Ile	Thr	Ser	Leu	Thr	Lys	Lys	Ser	Pro	Asn	Val	Lys	Ile	Gly	
75					80				85						90	
aat	atc	ggc	ttt	tca	att	gaa	aaa	aga	aat	att	cct	gtg	ctt	tac	ttc	819
Asn	Ile	Gly	Phe	Ser	Ile	Glu	Lys	Arg	Asn	Ile	Pro	Val	Leu	Tyr	Phe	
				95					100					105		
aca	aag	gac	aag	caa	ata	cgt	tcc	ata	tca	aaa	aaa	cca	acc	gtc	tgg	867
Thr	Lys	Asp	Lys	Gln	Ile	Arg	Ser	Ile	Ser	Lys	Lys	Pro	Thr	Val	Trp	
			110					115					120			
ctg	caa	gga	cag	ata	cat	gga	aat	gag	ccg	gca	gcg	gga	gaa	tct	gct	915
Leu	Gln	Gly	Gln	Ile	His	Gly	Asn	Glu	Pro	Ala	Ala	Gly	Glu	Ser	Ala	
		125					130					135				
ctg	gcg	ata	gct	gaa	aaa	ctg	gcc	gga	ccg	tat	ggc	gac	aaa	gtg	ttg	963
Leu	Ala	Ile	Ala	Glu	Lys	Leu	Ala	Gly	Pro	Tyr	Gly	Asp	Lys	Val	Leu	
	140					145					150					
gac	aag	atc	aat	gtc	atc	gtt	gtt	ccg	cgg	gtc	aat	cct	gac	gga	tca	1011
Asp	Lys	Ile	Asn	Val	Ile	Val	Val	Pro	Arg	Val	Asn	Pro	Asp	Gly	Ser	
155					160					165					170	
tat	cag	ttc	aac	aga	cgg	ctg	gcg	aac	gga	atc	gac	gga	aac	agg	gat	1059
Tyr	Gln	Phe	Asn	Arg	Arg	Leu	Ala	Asn	Gly	Ile	Asp	Gly	Asn	Arg	Asp	
				175					180					185		
cat	gtc	aag	ctc	gag	tct	cca	gaa	gtg	cgc	gcc	att	cac	caa	gaa	ttc	1107
His	Val	Lys	Leu	Glu	Ser	Pro	Glu	Val	Arg	Ala	Ile	His	Gln	Glu	Phe	
			190					195					200			
aat	aag	tat	tcg	cct	gaa	gtc	gtt	atc	gat	gcc	cat	gaa	tac	ggt	gtc	1155
Asn	Lys	Tyr	Ser	Pro	Glu	Val	Val	Ile	Asp	Ala	His	Glu	Tyr	Gly	Val	
		205					210					215				
ggc	caa	aac	gaa	ttt	cag	agc	ata	ggc	gaa	aaa	ggg	tca	tta	aaa	tac	1203
Gly	Gln	Asn	Glu	Phe	Gln	Ser	Ile	Gly	Glu	Lys	Gly	Ser	Leu	Lys	Tyr	
	220					225					230					
cat	gat	att	tta	att	tta	tca	gga	aaa	aat	tta	aac	att	ccc	aag	tcg	1251
His	Asp	Ile	Leu	Ile	Leu	Ser	Gly	Lys	Asn	Leu	Asn	Ile	Pro	Lys	Ser	
235					240					245					250	
atc	agg	cat	gcg	tcc	gac	agc	ctt	tat	gtg	aac	ggc	gtc	aga	gct	aaa	1299
Ile	Arg	His	Ala	Ser	Asp	Ser	Leu	Tyr	Val	Asn	Gly	Val	Arg	Ala	Lys	
				255					260					265		
ctt	gat	gaa	aaa	gga	ttt	tct	aat	gat	gct	tat	tat	acg	aca	gga	aaa	1347
Leu	Asp	Glu	Lys	Gly	Phe	Ser	Asn	Asp	Ala	Tyr	Tyr	Thr	Thr	Gly	Lys	
			270					275					280			
agc	aag	gac	gga	aaa	atc	gaa	atc	tat	gaa	ggc	ggt	aca	gaa	gcg	aga	1395
Ser	Lys	Asp	Gly	Lys	Ile	Glu	Ile	Tyr	Glu	Gly	Gly	Thr	Glu	Ala	Arg	
		285					290					295				
atc	ggg	cgt	aat	gca	ttc	gcc	ctc	cag	cct	gcc	ctt	tcc	ttc	ctg	gtg	1443
Ile	Gly	Arg	Asn	Ala	Phe	Ala	Leu	Gln	Pro	Ala	Leu	Ser	Phe	Leu	Val	
	300					305					310					
gaa	agc	agg	gga	ata	gac	atc	gga	cgc	gaa	aat	ttt	gca	aga	aga	gtc	1491
Glu	Ser	Arg	Gly	Ile	Asp	Ile	Gly	Arg	Glu	Asn	Phe	Ala	Arg	Arg	Val	
315					320					325					330	
gcg	gct	cag	gtt	gct	aca	cat	gag	acg	atc	atc	gac	acg	aca	gtg	aag	1539

10294.000.ST25.txt

Ala Ala Gln Val Ala Thr His Glu Thr Ile Ile Asp Thr Thr Val Lys
335 340 345

cat gca gcc gag atc aag cgc ctt gtc tcc aaa gaa aaa tta aag ctg 1587
His Ala Ala Glu Ile Lys Arg Leu Val Ser Lys Glu Lys Leu Lys Leu
350 355 360

ata caa aac ggc gct aaa gtg agc gat aaa gac caa gtg gtc atc aac 1635
Ile Gln Asn Gly Ala Lys Val Ser Asp Lys Asp Gln Val Val Ile Asn
365 370 375

agt gag ttt gca ggc ccg ttt aaa gac acg ctt aaa gtc gct gat att 1683
Ser Glu Phe Ala Gly Pro Phe Lys Asp Thr Leu Lys Val Ala Asp Ile
380 385 390

gcc tca gga caa gca gtt gac gtt cct gtc caa tat tac agc gcc tca 1731
Ala Ser Gly Gln Ala Val Asp Val Pro Val Gln Tyr Tyr Ser Ala Ser
395 400 405 410

gag gcc gtt cct gtg ctg tca aga act cgg ccg acc gct tac ctt gtc 1779
Glu Ala Val Pro Val Leu Ser Arg Thr Arg Pro Thr Ala Tyr Leu Val
415 420 425

ctt ccg ggc cat caa gat atc gaa cag aag ctg aag gat cag gga tta 1827
Leu Pro Gly His Gln Asp Ile Glu Gln Lys Leu Lys Asp Gln Gly Leu
430 435 440

aag agc gtg aca ctg gct ttc aaa caa aaa ctc acc gct gaa gcg tat 1875
Lys Ser Val Thr Leu Ala Phe Lys Gln Lys Leu Thr Ala Glu Ala Tyr
445 450 455

gag gtt tta tcg aaa gaa aca gcg gga gaa tct gag ggc cgg cca gtg 1923
Glu Val Leu Ser Lys Glu Thr Ala Gly Glu Ser Glu Gly Arg Pro Val
460 465 470

atc aag gta gaa acg aag ctc aaa aaa cag aaa aaa gag ttt cct aaa 1971
Ile Lys Val Glu Thr Lys Leu Lys Lys Gln Lys Lys Glu Phe Pro Lys
475 480 485 490

gga aca aaa atc tat ttt aca gct cag cag caa agc aat ctg ctg tca 2019
Gly Thr Lys Ile Tyr Phe Thr Ala Gln Gln Gln Ser Asn Leu Leu Ser
495 500 505

atc gca ctt gag ccg gag tcg gtt gac agt tat gta agc aca ggt tac 2067
Ile Ala Leu Glu Pro Glu Ser Val Asp Ser Tyr Val Ser Thr Gly Tyr
510 515 520

att cct tct caa aaa ggc aaa gag ctg ccg gtt tac cgc ttc atg ctg 2115
Ile Pro Ser Gln Lys Gly Lys Glu Leu Pro Val Tyr Arg Phe Met Leu
525 530 535

aac acc aaa acg ctt aat ttt aag gaa taatcaccag gcatccgtct 2162
Asn Thr Lys Thr Leu Asn Phe Lys Glu
540 545

ttgacggatg ctttttagcg gttttttgtt ttttcataca taattgtttt aaactgagat 2222

cgaaacctat acaataaata tcagtctgaa atctggaagg agagaatccg gttggaatca 2282

catgaagaat tatggaggga agccaaggcc ttcacgcgac tctgctacgg ggaactgtcg 2342

aagtccgaag aagaaacaag gatgcgctta cataaaatag ataaagaaat cagagaaacc 2402

ggaagctata cacatacatt agaagaaatc gaacatggag ccagaatggc gtggagaaac 2462

agcagccgct gcatcggcag gctgttttgg cactctctta ctgtcatcga tcaaagaggc 2522

gttcaaaccg aggcagaggt gcgggatgcg cttttccacc atattcagct tgcaacaaac 2582

10294.000.ST25.txt

ggaggggaaaa tcagaccgtt cattacgggtt ttcccccccg aacaaaacgg acacagcgaa 2642
gt 2644

<210> 166

<211> 547

<212> PRT

<213> Bacillus licheniformis

<400> 166

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20 25 30

Tyr Tyr Gly Lys Asn Tyr Thr Gln Pro Glu Gln Val Ser Ser Leu Tyr
35 40 45

Pro Glu Pro Glu Glu Thr Phe Ser Thr Pro Ala Phe Val Lys Glu Gly
50 55 60

Glu Ala Phe Thr Thr Gln Glu Glu Met Met Lys Phe Ile Thr Ser Leu
65 70 75 80

Thr Lys Lys Ser Pro Asn Val Lys Ile Gly Asn Ile Gly Phe Ser Ile
85 90 95

Glu Lys Arg Asn Ile Pro Val Leu Tyr Phe Thr Lys Asp Lys Gln Ile
100 105 110

Arg Ser Ile Ser Lys Lys Pro Thr Val Trp Leu Gln Gly Gln Ile His
115 120 125

Gly Asn Glu Pro Ala Ala Gly Glu Ser Ala Leu Ala Ile Ala Glu Lys
130 135 140

Leu Ala Gly Pro Tyr Gly Asp Lys Val Leu Asp Lys Ile Asn Val Ile
145 150 155 160

Val Val Pro Arg Val Asn Pro Asp Gly Ser Tyr Gln Phe Asn Arg Arg
165 170 175

Leu Ala Asn Gly Ile Asp Gly Asn Arg Asp His Val Lys Leu Glu Ser
180 185 190

Pro Glu Val Arg Ala Ile His Gln Glu Phe Asn Lys Tyr Ser Pro Glu
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Val Val Ile Asp Ala His Glu Tyr Gly Val Gly Gln Asn Glu Phe Gln
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 225 230 235 240
 Ser Gly Lys Asn Leu Asn Ile Pro Lys Ser Ile Arg His Ala Ser Asp
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 Ser Leu Tyr Val Asn Gly Val Arg Ala Lys Leu Asp Glu Lys Gly Phe
 260 265 270
 Ser Asn Asp Ala Tyr Tyr Thr Thr Gly Lys Ser Lys Asp Gly Lys Ile
 275 280 285
 Glu Ile Tyr Glu Gly Gly Thr Glu Ala Arg Ile Gly Arg Asn Ala Phe
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 Ile Gly Arg Glu Asn Phe Ala Arg Arg Val Ala Ala Gln Val Ala Thr
 325 330 335
 His Glu Thr Ile Ile Asp Thr Thr Val Lys His Ala Ala Glu Ile Lys
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 Val Ser Asp Lys Asp Gln Val Val Ile Asn Ser Glu Phe Ala Gly Pro
 370 375 380
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 Ser Arg Thr Arg Pro Thr Ala Tyr Leu Val Leu Pro Gly His Gln Asp
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 Ile Glu Gln Lys Leu Lys Asp Gln Gly Leu Lys Ser Val Thr Leu Ala
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Leu Lys Lys Gln Lys Lys Glu Phe Pro Lys Gly Thr Lys Ile Tyr Phe
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Thr Ala Gln Gln Gln Ser Asn Leu Leu Ser Ile Ala Leu Glu Pro Glu
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ser Val Asp Ser Tyr Val Ser Thr Gly Tyr Ile Pro Ser Gln Lys Gly
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<220>

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<222> (501)..(1643)

<223>

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 Met Asn Phe Tyr Lys Thr Leu Ala Leu Ser Thr
 1 5 10
 ctt gcg gca tcc tta ttg tct ccc tca tgg agc att ctc ccc cgt gcc 581
 Leu Ala Ala Ser Leu Leu Ser Pro Ser Trp Ser Ile Leu Pro Arg Ala
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Pro	His	Leu	Thr	Ala	Asp	Ile	Glu	Gly	Leu	Thr	Ile	Tyr	Tyr	Gly	Glu		
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320      325
gtc gcc caa gac ggc gaa aat acg gaa aat gga cag cca gcc aat cag 1541
Val Ala Gln Asp Gly Glu Asn Thr Glu Asn Gly Gln Pro Ala Asn Gln
335      340
aac ttc aaa att gtc tcc tgg gaa aaa att gct gac gcg ctg gac gac 1589
Asn Phe Lys Ile Val Ser Trp Glu Lys Ile Ala Asp Ala Leu Asp Asp
350      355      360
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Lys Pro Asp Ile Asp Asp Gln Val Asn Pro Arg Lys Leu Lys Lys Arg
365      370      375
gcc aaa taacgacgga tccgcgggaa atgcccgcgg atttttcaca ttcctttatg 1693
Ala Lys
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<211> 381

<212> PRT

<213> Bacillus licheniformis

<400> 168

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35      40      45
Pro Asp Asp Ala Ala Asp Asp Pro Ala Ile Trp Val His Pro Lys Gln
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 Ile Asp Ile Ala Gly Ala Ser Asn Arg Ser Asp Gly Lys Asn Thr Val
 115 120 125
 Glu Ile Tyr Ala Phe Asp Gly Glu Lys Asn Lys Leu Lys Asn Ile Val
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 Asn Pro Gln Lys Pro Ile Gln Thr Asp Ile Glu Glu Val Tyr Gly Phe
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 Ser Leu Tyr His Ser Gln Lys Thr Gly Lys Phe Tyr Ala Met Val Thr
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 Gly Lys Asn Gly Glu Phe Glu Gln Tyr Glu Leu Phe Asp Asn Gly Lys
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 Gly Gln Val Glu Gly Lys Lys Val Arg Ser Phe Lys Met Ser Ser Gln
 195 200 205
 Thr Glu Gly Leu Ala Ala Asp Asp Glu Tyr Gly Lys Met Tyr Ile Ala
 210 215 220
 Glu Glu Asp Ala Ala Ile Trp Ser Phe Ser Ala Glu Pro Asn Gly Gly
 225 230 235 240
 Asp Lys Gly Lys Ile Val Asp Arg Ala Gly Gly Pro His Leu Thr Ala
 245 250 255
 Asp Ile Glu Gly Leu Thr Ile Tyr Tyr Gly Glu Asp Gly Glu Gly Tyr
 260 265 270
 Leu Ile Ala Ser Ser Gln Gly Asp Asn Arg Tyr Ala Ile Tyr Asp Arg
 275 280 285
 Arg Gly Lys Asn Asp Tyr Val Ala Asp Phe Ser Ile Asp Asp Gly Lys
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 Glu Ile Asp Gly Thr Ser Asp Thr Asp Gly Ile Asp Val Ile Gly Phe
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 Gly Leu Gly Lys Lys Tyr Pro Tyr Gly Ile Phe Val Ala Gln Asp Gly
 325 330 335

Glu Asn Thr Glu Asn Gly Gln Pro Ala Asn Gln Asn Phe Lys Ile Val
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Ser Trp Glu Lys Ile Ala Asp Ala Leu Asp Asp Lys Pro Asp Ile Asp
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Asp Gln Val Asn Pro Arg Lys Leu Lys Lys Arg Ala Lys
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<212> DNA

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Met Lys Arg Val Ile Val Leu Phe Ser Ile Leu	
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Leu Ala Leu Phe Ile Val Tyr Tyr Asp Leu Lys Ser Gly Thr Ile Pro	
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caa aac gcc tta ccg gct tca acc atg gca gcg gaa gct ccg gct gca	629
Gln Asn Ala Leu Pro Ala Ser Thr Met Ala Ala Glu Ala Pro Ala Ala	
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agc ctg caa tat aag tcc gtt acg gta aag ccc gga caa acg gta ttt	677
Ser Leu Gln Tyr Lys Ser Val Thr Val Lys Pro Gly Gln Thr Val Phe	
45 50 55	
tca atc atc ggg aac agc gcc gtt ccg gct gac aaa ata gcc gaa gat	725
Ser Ile Ile Gly Asn Ser Ala Val Pro Ala Asp Lys Ile Ala Glu Asp	
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gtc acc tac aag ttt ccc gtt tat cct gat taagcgtaa tttcttgtca 823
Val Thr Tyr Lys Phe Pro Val Tyr Pro Asp
95 100

gtttcatgaa cgggctgtta caataagact tgtaaacgat ttggtataag aaaaggagca 883

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tcgcggaagc aggatgtcaa atcgtccgcg tcgcctgtcc tgatgaacgg gctgccgacg 1123

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ataaattggc attaaaagcg atcgaaggcg gagccgataa aatccgcac aatccgggta 1243

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<211> 101

<212> PRT

<213> Bacillus licheniformis

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Ser Val Thr Val Lys Pro Gly Gln Thr Val Phe Ser Ile Ile Gly Asn
50 55 60

Ser Ala Val Pro Ala Asp Lys Ile Ala Glu Asp Phe Glu Glu Leu Asn
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<211> 1627

<212> DNA

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<222> (501)..(1124)

<223>

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10294.000.ST25.txt

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Glu Val Ala Ile Pro Phe Phe Ser Tyr Gly Gly Asp Thr Lys Val Ala
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Gly Lys Asp Gly Ser Tyr Thr Val Tyr Glu Phe Val Gly Asp Gln Asn
115 120 125

Asp Gly Pro Val Ser Tyr Gln Lys Asn Tyr Gln Thr Val Thr Leu Lys
130 135 140

Asn Thr Gly Gly Ser Phe Lys Val Thr Asp Ile Gly Gln Ser Asp Thr
145 150 155 160

Lys Pro Ala Gly Glu Glu Ile Met Ser Lys Gln Pro Asp Glu Lys Glu
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<212> DNA

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<223>

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tcccactacc ttgaaatgaa agcgctggag aacaataagc ggcaagtgct ccacggtgct 180
aaagtcggct gcagcgcgat tatgctgact gacatttacc gatctcttat cggtgcaagc 240
ctgggtgata aacacgctga gcaagcgatt cgctccgttt atgaaaagct ccctgacggg 300
aagaaaatgg cagagtggat gaggcgtatc ggcgggcctg tatcattcaa agaactcgat 360

420
480
533

581

629

677

725

773

821

869

917

965

1013

1061

1109

1157

1205

1253

gttgaagaag agctgggtgag agaagcgcctc gcatacgcgcc atcagctcag agaccggtat															
acggggactga aaatcatcaa tcaatacggc cttttgccgg ggcttttagg caaaggacca															
ggcgtgaaag gggttaaaaat gtg aaa agg ttc ctt tca tct atc ttt atg gtc															
Val Lys Arg Phe Leu Ser Ser Ile Phe Met Val															
1 5 10															
acg gtc gct gta tgt ttg ctt tta tcg ggg tgc aag gcg agt cct gcc															
Thr Val Ala Val Cys Leu Leu Leu Ser Gly Cys Lys Ala Ser Pro Ala															
15 20 25															
tcc gat caa gcg gac ggc acc gaa ctg aca ttt tgg aca ttc aac ggc															
Ser Asp Gln Ala Asp Gly Thr Glu Leu Thr Phe Trp Thr Phe Asn Gly															
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ctt cat gaa cag ttt tat gct gag atg gtg aaa gaa tgg aac aaa aag															
Leu His Glu Gln Phe Tyr Ala Glu Met Val Lys Glu Trp Asn Lys Lys															
45 50 55															
tat ccc gag cga aaa atc aaa tta aat aca gtg gtg tat ccg tat gga															
Tyr Pro Glu Arg Lys Ile Lys Leu Asn Thr Val Val Tyr Pro Tyr Gly															
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cag atg cat gac aat tta tct atc tcg ctt tta gcc ggg aaa ggg gtt															
Gln Met His Asp Asn Leu Ser Ile Ser Leu Leu Ala Gly Lys Gly Val															
80 85 90															
cca gat att gcc gat gtt gag ctg ggg cgc tat tcg aac ttt ttg aag															
Pro Asp Ile Ala Asp Val Glu Leu Gly Arg Tyr Ser Asn Phe Leu Lys															
95 100 105															
ggc tct gac att cct ctt acc gat tta acg ccg ctt gtg gag gac gaa															
Gly Ser Asp Ile Pro Leu Thr Asp Leu Thr Pro Leu Val Glu Asp Glu															
110 115 120															
cgc gac aag ttt gtt gaa gcg agg ctg acg ctc tac agc aag aac ggc															
Arg Asp Lys Phe Val Glu Ala Arg Leu Thr Leu Tyr Ser Lys Asn Gly															
125 130 135															
aag ctt tac gga ctt gac aca cat gtc gga act acc gtg atg tat tac															
Lys Leu Tyr Gly Leu Asp Thr His Val Gly Thr Thr Val Met Tyr Tyr															
140 145 150 155															
aac atg gaa atg atg aat aaa gca ggc gtt gat ccg gac gac atc aaa															
Asn Met Glu Met Met Asn Lys Ala Gly Val Asp Pro Asp Asp Ile Lys															
160 165 170															
aca tgg gaa gat tac agg gaa gcg ggc aaa aag gtc gtc aaa gct ctc															
Thr Trp Glu Asp Tyr Arg Glu Ala Gly Lys Lys Val Val Lys Ala Leu															
175 180 185															
gga aag ccg atg acg acg att gaa acg acc gac ccg aat tca ttt ctg															
Gly Lys Pro Met Thr Thr Ile Glu Thr Thr Asp Pro Asn Ser Phe Leu															
190 195 200															
ccg ctg gtt tcc cag cag gga tcc ggt tac ttt gat gag cag ggg cgg															
Pro Leu Val Ser Gln Gln Gly Ser Ser Tyr Phe Asp Glu Gln Gly Arg															
205 210 215															
ttg aca tta aac aat gag aca aac gtg aaa acg ctc gaa ttt tta aag															
Leu Thr Leu Asn Asn Glu Thr Asn Val Lys Thr Leu Glu Phe Leu Lys															
220 225 230 235															
act tta att gag aaa gac aaa att gcc gtc aca acg ccc gga ggc aat															
Thr Leu Ile Glu Lys Asp Lys Ile Ala Val Thr Thr Pro Gly Gly Asn															
240 245 250															

10294.000.ST25.txt

cat cac agt gaa gag tat tac gga ttt atg aac caa ggc ggc gcg gcg His His Ser Glu Glu Tyr Tyr Gly Phe Met Asn Gln Gly Gly Ala Ala	1301
tct gtc tta atg ccg atc tgg tat atg ggc cgt ttt ttg gat tat atg Ser Val Leu Met Pro Ile Trp Tyr Met Gly Arg Phe Leu Asp Tyr Met	1349
cct gac ttg aaa ggg aaa atc gcg atc aga ccg ctg ccg gca tgg gaa Pro Asp Leu Lys Gly Lys Ile Ala Ile Arg Pro Leu Pro Ala Trp Glu	1397
gaa ggg gga gac cgc tca gcg gga atg ggc gga acg gcc acc gtg att Glu Gly Gly Asp Arg Ser Ala Gly Met Gly Gly Thr Ala Thr Val Ile	1445
cca aaa cag gcg aaa cag gtc gat ctg gcc aag gat ttc ttg aaa ttt Pro Lys Gln Ala Lys Gln Val Asp Leu Ala Lys Asp Phe Leu Lys Phe	1493
gcc aaa gcg tca aaa gaa ggc aac atc aag ctg tgg acc gtg ctc ggg Ala Lys Ala Ser Lys Glu Gly Asn Ile Lys Leu Trp Thr Val Leu Gly	1541
ttc gat ccg ctc aga tgg gat gtg tgg gac tcg gac gaa ttg aaa aaa Phe Asp Pro Leu Arg Trp Asp Val Trp Asp Ser Asp Glu Leu Lys Lys	1589
cca aat caa tat aca gaa tac ttt caa aac gga caa cac atc ttt tcc Pro Asn Gln Tyr Thr Glu Tyr Phe Gln Asn Gly Gln His Ile Phe Ser	1637
gtg ctt ctt gac ata aag gat gag atc aat ccg ctt tac ctt act gag Val Leu Leu Asp Ile Lys Asp Glu Ile Asn Pro Leu Tyr Leu Thr Glu	1685
gat tat gcg aag act tcc gat ctc gtc aac aga aac ata ctg tac gaa Asp Tyr Ala Lys Thr Ser Asp Leu Val Asn Arg Asn Ile Leu Tyr Glu	1733
gcg ctc aaa acg aag agc aaa aca ccg aaa gaa gca ttg gac aaa gca Ala Leu Lys Thr Lys Ser Lys Thr Pro Lys Glu Ala Leu Asp Lys Ala	1781
gca gct gaa gtg aaa ggg caa tagtctttca ttactgtaaa gcgagggcat Ala Ala Glu Val Lys Gly Gln	1832
aacttgaaga ctgttaaaac agatacagtg cattcgtttc cgccggtgag cagaaaaaga	1892
aagatcagac gtttattata ttcagcaaaa gccgcaccct acatttttac agcacctttt	1952
gtactctcct ttgcatatt ttttctttat ccgcttatca gcgtcgtcat catgagtttt	2012
caaagcattc tccccgggga agtccgcttc atcgggacgg agaactataa agcattaaac	2072
aatcctacat ttatatccgc actattcaac accgtaaaat acaccttttg gacattgctg	2132
attttaatac ctgttcctct tattctggca gtcttttttag attctaaact cgtaaagttt	2192
aaaaacgtgt tcaaatcggc tttattcatc ccggctctga cttcaaccat tgtggcgggg	2252
attattttca ggctgatttt tggagaaatg gatacatccc tggcg	2297

<210> 174

<211> 434

<212> PRT

<213> Bacillus licheniformis

<400> 174

Val Lys Arg Phe Leu Ser Ser Ile Phe Met Val Thr Val Ala Val Cys
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Leu Leu Leu Ser Gly Cys Lys Ala Ser Pro Ala Ser Asp Gln Ala Asp
 20 25 30

Gly Thr Glu Leu Thr Phe Trp Thr Phe Asn Gly Leu His Glu Gln Phe
 35 40 45

Tyr Ala Glu Met Val Lys Glu Trp Asn Lys Lys Tyr Pro Glu Arg Lys
 50 55 60

Ile Lys Leu Asn Thr Val Val Tyr Pro Tyr Gly Gln Met His Asp Asn
 65 70 75 80

Leu Ser Ile Ser Leu Leu Ala Gly Lys Gly Val Pro Asp Ile Ala Asp
 85 90 95

Val Glu Leu Gly Arg Tyr Ser Asn Phe Leu Lys Gly Ser Asp Ile Pro
 100 105 110

Leu Thr Asp Leu Thr Pro Leu Val Glu Asp Glu Arg Asp Lys Phe Val
 115 120 125

Glu Ala Arg Leu Thr Leu Tyr Ser Lys Asn Gly Lys Leu Tyr Gly Leu
 130 135 140

Asp Thr His Val Gly Thr Thr Val Met Tyr Tyr Asn Met Glu Met Met
 145 150 155 160

Asn Lys Ala Gly Val Asp Pro Asp Asp Ile Lys Thr Trp Glu Asp Tyr
 165 170 175

Arg Glu Ala Gly Lys Lys Val Val Lys Ala Leu Gly Lys Pro Met Thr
 180 185 190

Thr Ile Glu Thr Thr Asp Pro Asn Ser Phe Leu Pro Leu Val Ser Gln
 195 200 205

Gln Gly Ser Gly Tyr Phe Asp Glu Gln Gly Arg Leu Thr Leu Asn Asn
 210 215 220

Glu Thr Asn Val Lys Thr Leu Glu Phe Leu Lys Thr Leu Ile Glu Lys
 225 230 235 240

Asp Lys Ile Ala Val Thr Thr Pro Gly Gly Asn His His Ser Glu Glu
 245 250 255
 Tyr Tyr Gly Phe Met Asn Gln Gly Gly Ala Ala Ser Val Leu Met Pro
 260 265 270
 Ile Trp Tyr Met Gly Arg Phe Leu Asp Tyr Met Pro Asp Leu Lys Gly
 275 280 285
 Lys Ile Ala Ile Arg Pro Leu Pro Ala Trp Glu Glu Gly Gly Asp Arg
 290 295 300
 Ser Ala Gly Met Gly Gly Thr Ala Thr Val Ile Pro Lys Gln Ala Lys
 305 310 315 320
 Gln Val Asp Leu Ala Lys Asp Phe Leu Lys Phe Ala Lys Ala Ser Lys
 325 330 335
 Glu Gly Asn Ile Lys Leu Trp Thr Val Leu Gly Phe Asp Pro Leu Arg
 340 345 350
 Trp Asp Val Trp Asp Ser Asp Glu Leu Lys Lys Pro Asn Gln Tyr Thr
 355 360 365
 Glu Tyr Phe Gln Asn Gly Gln His Ile Phe Ser Val Leu Leu Asp Ile
 370 375 380
 Lys Asp Glu Ile Asn Pro Leu Tyr Leu Thr Glu Asp Tyr Ala Lys Thr
 385 390 395 400
 Ser Asp Leu Val Asn Arg Asn Ile Leu Tyr Glu Ala Leu Lys Thr Lys
 405 410 415
 Ser Lys Thr Pro Lys Glu Ala Leu Asp Lys Ala Ala Ala Glu Val Lys
 420 425 430

Gly Gln

<210> 175

<211> 1864

<212> DNA

<213> *Bacillus licheniformis*

<220>

<221> CDS

<222> (533)..(991)

<223>

<400> 175

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gcc	agtc	cagc	cttct	gttg	aa	cg	gcttg	tg	agatt	ccc	cg	ccttc	gtt	ctt	ta	agcat	120
tac	ggg	cg	gag	ccgat	gc	tct	catt	aaa	atct	gt	aaag	ga	atat	gt	ctg	ttc	180
aaa	at	ac	gct	cat	ga	ac	gc	gcgt	gc	gac	at	caac	tcaa	act	tga	cg	240
cg	gcc	gct	ac	gag	ct	gat	ca	tccc	ct	ac	ct	ac	ct	ac	ct	ac	300
aa	cg	gt	cg	aa	aa	aa	aa	aa	aa	aa	aa	aa	aa	aa	aa	aa	360
ac	ag	cg	gg	gc	cg	ct	att	tc	g	aaaa	at	gat	cg	aaa	ac	gc	420
gg	t	cat	gg	tc	tcc	gc	cg	gag	a	caa	ac	gc	gc	g	ct	t	480
tc	acc	gc	g	caa	att	gt	c	ga	ag	ac	at	g	aa	at	g	cg	538
ccg	agc	gac	ttt	gca	agc	gca	ctt	gaa	tct	tta	agc	tta	aaa	gac	atg		586
Pro	Ser	Asp	Phe	Ala	Ser	Ala	Leu	Glu	Ser	Leu	Ser	Leu	Lys	Asp	Met		
		5					10					15					
aga	aaa	gcg	atc	cac	cg	ctt	ctt	gac	att	cg	gac	gaa	aat	acg	tgg		634
Arg	Lys	Ala	Ile	His	Arg	Leu	Leu	Asp	Ile	Arg	Asp	Glu	Asn	Thr	Trp		
	20					25					30						
atg	ctg	ttc	ggc	act	ctg	ccg	ttt	tac	gcg	tgc	agc	cct	gat	cct	gaa		682
Met	Leu	Phe	Gly	Thr	Leu	Pro	Phe	Tyr	Ala	Cys	Ser	Pro	Asp	Pro	Glu		
	35				40				45						50		
gat	cac	gcc	ctc	tta	cag	cg	ctg	cg	gaa	gcg	aaa	aac	gtc	acc	gtc		730
Asp	His	Ala	Leu	Leu	Gln	Arg	Leu	Arg	Glu	Ala	Lys	Asn	Val	Thr	Val		
			55						60					65			
aga	aac	gac	cct	gac	ggc	aga	tcg	cg	ctg	aac	gtc	aat	att	ttt	gac		778
Arg	Asn	Asp	Pro	Asp	Gly	Arg	Ser	Arg	Leu	Asn	Val	Asn	Ile	Phe	Asp		
			70				75						80				
ggc	aat	atc	atc	gtg	acc	gat	ttc	gga	gat	act	ccg	ccg	ctc	ggc	aac		826
Gly	Asn	Ile	Ile	Val	Thr	Asp	Phe	Gly	Asp	Thr	Pro	Pro	Leu	Gly	Asn		
		85					90					95					
att	cag	aca	gac	agc	ctg	cca	agc	gcc	tac	gcg	aag	tgg	aga	aaa	aca		874
Ile	Gln	Thr	Asp	Ser	Leu	Pro	Ser	Ala	Tyr	Ala	Lys	Trp	Arg	Lys	Thr		
	100					105					110						
gag	ctt	gcc	aaa	gaa	ctc	aac	tgc	cac	tgc	ccg	cac	gtc	cg	tgc	ctc		922
Glu	Leu	Ala	Lys	Glu	Leu	Asn	Cys	His	Cys	Pro	His	Val	Arg	Cys	Leu		
	115				120					125					130		
gga	ccg	aat	gtg	ctc	gtc	aaa	aac	agc	tat	tat	caa	gat	gtt	gat	ttt		970
Gly	Pro	Asn	Val	Leu	Val	Lys	Asn	Ser	Tyr	Tyr	Gln	Asp	Val	Asp	Phe		
				135					140					145			
act	tcc	aga	aca	gca	aga	gta	tg	aaaa	aa	gc	aag	cc	gc	aaa	gg		1021
Thr	Ser	Arg	Thr	Ala	Arg	Val											
			150														
ttt	att	tc	gc	g	ct	gat	gg	ct	g	ag	ct	g	aa	ag	c		1081

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aagcgccgat tccttgcgag gtgatatttt tgacgactag ctttcttttg ttgcctttta 1141
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 cgtgtaaatt tcccagtttt ttcggctgca ctttataaat ctgatcgcg tttgtaccgg 1261
 agccgaccac tgtttcaaag gcgagcggca gctttgtttt ttccatggct ttgagcatca 1321
 tcatattttt gacatcttcc gcctttggaa ctttcgctgt taagccgcct ttgattttgc 1381
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 gcgccccatct gcccaaataa atcgtcgccc gatagccgat tgccagcggg gtgccggaaa 1561
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 tcagcagctc ttcggctaata tcgctcggct gcagcctcgg ctgatcctga gaggcgtag 1681
 ggtatgtgtt ctctttggaa atattcgta cagagcttgg aatcttgatc ggcttggtg 1741
 cgtcagcttc ctgtacagcg aaaaaactaa aggataaaaa cgcagtcagc gtaaaacaca 1801
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 tct 1864

<210> 176

<211> 153

<212> PRT

<213> Bacillus licheniformis

<400> 176

Met Tyr Pro Ser Asp Phe Ala Ser Ala Leu Glu Ser Leu Ser Leu Lys
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Asp Met Arg Lys Ala Ile His Arg Leu Leu Asp Ile Arg Asp Glu Asn
 20 25 30

Thr Trp Met Leu Phe Gly Thr Leu Pro Phe Tyr Ala Cys Ser Pro Asp
 35 40 45

Pro Glu Asp His Ala Leu Leu Gln Arg Leu Arg Glu Ala Lys Asn Val
 50 55 60

Thr Val Arg Asn Asp Pro Asp Gly Arg Ser Arg Leu Asn Val Asn Ile
 65 70 75 80

Phe Asp Gly Asn Ile Ile Val Thr Asp Phe Gly Asp Thr Pro Pro Leu
 85 90 95

Gly Asn Ile Gln Thr Asp Ser Leu Pro Ser Ala Tyr Ala Lys Trp Arg
 100 105 110

10294.000.ST25.txt

Lys Thr Glu Leu Ala Lys Glu Leu Asn Cys His Cys Pro His Val Arg
 115 120 125

Cys Leu Gly Pro Asn Val Leu Val Lys Asn Ser Tyr Tyr Gln Asp Val
 130 135 140

Asp Phe Thr Ser Arg Thr Ala Arg Val
 145 150

<210> 177

<211> 1763

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (503)..(1264)

<223>

<400> 177
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 cacactcaaa tgtgcgatgt ataaaaatga attaacaggt acgtttttgtc ttgttttagtt 240
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 ttgtcaataa cttttctcaa aattatTTTT tggagctttt tcatgtcagc tgtttatcag 360
 cgacgaataa caatataaca tgtttattta attccgggtca accctctttt taattttttt 420
 ctttaagatga attattgtta tgttctatTT taaacaagca taggatgaaa acaaagcagc 480
 atggacaagg aggagttttt ct gtg aac cat ttt tat gtg tgg cat atc aaa 532
 Val Asn His Phe Tyr Val Trp His Ile Lys
 1 5 10
 cgg att aag cag cta atc att att atg ata gcc gct ttt gcg aca gca 580
 Arg Ile Lys Gln Leu Ile Ile Ile Met Ile Ala Ala Phe Ala Thr Ala
 15 20 25
 agt ttt ttt tat gtg caa aac ctg ctc cct ctt cct gtg ttt tct aca 628
 Ser Phe Phe Tyr Val Gln Asn Leu Leu Pro Leu Pro Val Phe Ser Thr
 30 35 40
 gaa ggc gga gca aaa gcg gta tat aga gga gat tca gat aca aat gaa 676
 Glu Gly Gly Ala Lys Ala Val Tyr Arg Gly Asp Ser Asp Thr Asn Glu
 45 50 55
 gta gcc ctt aca ttt aat atc agc tgg gga gat caa aag gca atg ccc 724

10294.000.ST25.txt

Val	Ala	Leu	Thr	Phe	Asn	Ile	Ser	Trp	Gly	Asp	Gln	Lys	Ala	Met	Pro		
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Ile	Leu	Asp	Thr	Leu	Lys	Ala	Asn	Gly	Ile	Lys	Asp	Ala	Thr	Phe	Phe		
75					80					85				90			
cta	tca	gct	tca	tgg	gca	gag	cgc	cac	ccg	gat	gtc	gta	gaa	aga	atc	820	
Leu	Ser	Ala	Ser	Trp	Ala	Glu	Arg	His	Pro	Asp	Val	Val	Glu	Arg	Ile		
				95					100					105			
cgt	aaa	gat	ggt	cac	cag	atc	ggg	agt	atg	ggc	tat	gct	tat	aaa	aac	868	
Arg	Lys	Asp	Gly	His	Gln	Ile	Gly	Ser	Met	Gly	Tyr	Ala	Tyr	Lys	Asn		
			110					115					120				
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Tyr	Ser	Gln	Met	Lys	Lys	Ser	Glu	Ile	Lys	Lys	Asp	Leu	Ala	Lys	Ala		
		125					130					135					
cga	cac	tcc	ttt	caa	aaa	ctc	ggg	ctt	gac	gac	ctt	acg	ctt	tta	aga	964	
Arg	His	Ser	Phe	Gln	Lys	Leu	Gly	Leu	Asp	Asp	Leu	Thr	Leu	Leu	Arg		
	140					145					150						
ccg	ccg	acc	ggc	cag	ttt	aat	aaa	gac	gta	ctc	gat	gtt	gct	aaa	cag	1012	
Pro	Pro	Thr	Gly	Gln	Phe	Asn	Lys	Asp	Val	Leu	Asp	Val	Ala	Lys	Gln		
155				160					165					170			
tac	ggc	tac	acc	gtt	gtt	cat	tat	agt	att	aac	tcg	gat	gac	tgg	acg	1060	
Tyr	Gly	Tyr	Thr	Val	Val	His	Tyr	Ser	Ile	Asn	Ser	Asp	Asp	Trp	Thr		
				175					180					185			
aac	ccg	ggg	gtt	caa	aag	atc	gtc	caa	aac	gta	aat	gga	acg	gta	aac	1108	
Asn	Pro	Gly	Val	Gln	Lys	Ile	Val	Gln	Asn	Val	Asn	Gly	Thr	Val	Asn		
			190				195					200					
gcc	ggt	gac	atc	gtg	ctc	ttt	cac	gct	tca	gat	tcc	gcc	aaa	caa	aca	1156	
Ala	Gly	Asp	Ile	Val	Leu	Phe	His	Ala	Ser	Asp	Ser	Ala	Lys	Gln	Thr		
		205					210					215					
aaa	gaa	gcc	ctg	cca	gag	atc	gtg	cac	cat	ctc	aga	agc	aag	ggg	ctc	1204	
Lys	Glu	Ala	Leu	Pro	Glu	Ile	Val	His	His	Leu	Arg	Ser	Lys	Gly	Leu		
	220					225					230						
aaa	aac	gta	aca	gtc	agc	gaa	tta	atc	gca	aat	acg	gat	gca	aaa	tct	1252	
Lys	Asn	Val	Thr	Val	Ser	Glu	Leu	Ile	Ala	Asn	Thr	Asp	Ala	Lys	Ser		
235					240				245					250			
tca	gaa	gta	aag	tagcagccgg	tctaagcgcg	tgcttgaaat	tttggcagca									1304	
Ser	Glu	Val	Lys														
ttaaaagctg	aaaagcgctg	caggctaata	aaggaagcag	cattaaatag	agccagtcct											1364	
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gaatcgaatt	ccacaaagaa	tgagatctga	aaatttccag	tgcaaagcgg	tgaatcgтта											1664	
agaaaatcac	aaatcccatt	tgagcaatca	cgctaaagat	catgccaacc	ccgataaacc											1724	
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<210> 178

<211> 254

<212> PRT

<213> Bacillus licheniformis

<400> 178

Val Asn His Phe Tyr Val Trp His Ile Lys Arg Ile Lys Gln Leu Ile
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Ile Ile Met Ile Ala Ala Phe Ala Thr Ala Ser Phe Phe Tyr Val Gln
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Asn Leu Leu Pro Leu Pro Val Phe Ser Thr Glu Gly Gly Ala Lys Ala
35 40 45

Val Tyr Arg Gly Asp Ser Asp Thr Asn Glu Val Ala Leu Thr Phe Asn
50 55 60

Ile Ser Trp Gly Asp Gln Lys Ala Met Pro Ile Leu Asp Thr Leu Lys
65 70 75 80

Ala Asn Gly Ile Lys Asp Ala Thr Phe Phe Leu Ser Ala Ser Trp Ala
85 90 95

Glu Arg His Pro Asp Val Val Glu Arg Ile Arg Lys Asp Gly His Gln
100 105 110

Ile Gly Ser Met Gly Tyr Ala Tyr Lys Asn Tyr Ser Gln Met Lys Lys
115 120 125

Ser Glu Ile Lys Lys Asp Leu Ala Lys Ala Arg His Ser Phe Gln Lys
130 135 140

Leu Gly Leu Asp Asp Leu Thr Leu Leu Arg Pro Pro Thr Gly Gln Phe
145 150 155 160

Asn Lys Asp Val Leu Asp Val Ala Lys Gln Tyr Gly Tyr Thr Val Val
165 170 175

His Tyr Ser Ile Asn Ser Asp Asp Trp Thr Asn Pro Gly Val Gln Lys
180 185 190

Ile Val Gln Asn Val Asn Gly Thr Val Asn Ala Gly Asp Ile Val Leu
195 200 205

Phe His Ala Ser Asp Ser Ala Lys Gln Thr Lys Glu Ala Leu Pro Glu
210 215 220

Ile Val His His Leu Arg Ser Lys Gly Leu Lys Asn Val Thr Val Ser
225 230 235 240

Glu Leu Ile Ala Asn Thr Asp Ala Lys Ser Ser Glu Val Lys
245 250

<210> 179

<211> 1610

<212> DNA

<213> *Bacillus licheniformis*

<220>

<221> CDS

<222> (501) . . (1304)

<223>

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aacgctgcgg gaaatgagcg ggaaagtccc tctgacagac gaagagcttt tgtcagtcaa    180
aggagtggga gaacaaaaa gagtaaaata cggagctgta tttctacagg agcttcaagc    240
ctataaaact gagaaagaag cataaaaacc caaaatttat atatgtaaaa ttttttttag    300
taaatctcct atttcagttg aaaaacgatt ggaacccttg atacatctga atttcggccg    360
attttagggc ggctgaaatt cctcctcgta aaacaactgt aatcaaaaac aaattgtttt    420
gttattgatt tgacattttc atatgttacg attgctcctg ttagccggac aataaaaagc    480
taacaaggga ggatttactt atg aag aag acg ttt atg tcc ttt gtt gca gtt    533
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gca gca tta tct tca act gca ttc gga gcg agt gcc tct gca aaa gaa      581
Ala Ala Leu Ser Ser Thr Ala Phe Gly Ala Ser Ala Ser Ala Lys Glu
                    15      20      25

gta aca gtc caa aaa ggt gac acc ctt tgg gga atc tcg caa aaa caa      629
Val Thr Val Gln Lys Gly Asp Thr Leu Trp Gly Ile Ser Gln Lys Gln
                    30      35      40

ggg gta aat ctg cag gac tta aaa gaa tgg aat cag ctt tcc tct gac      677
Gly Val Asn Leu Gln Asp Leu Lys Glu Trp Asn Gln Leu Ser Ser Asp
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ttg att att ccg gga caa aag ctg aac gtt tct gaa aaa cag aca gaa      725
Leu Ile Ile Pro Gly Gln Lys Leu Asn Val Ser Glu Lys Gln Thr Glu
                    60      65      70      75

gaa aag aaa caa tat acc att aaa aag gga gac act ctc tgg aaa atc      773
Glu Lys Lys Gln Tyr Thr Ile Lys Lys Gly Asp Thr Leu Trp Lys Ile
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10294.000.ST25.txt

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ata Ile	aaa Lys	tca Ser 110	gat Asp	atc Ile	att Ile	tac Tyr	ccg Pro 115	aat Asn	aca Thr	tcc Ser	ata Ile	act Thr 120	gtt Val	gac Asp	gga Gly	869														
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ggc Gly	ggt Gly	atg Met 190	aca Thr	ggc Gly	gtg Val	aca Thr	gcc Ala 195	acg Thr	ggt Gly	atc Ile	gat Asp	ctg Leu 200	aag Lys	gcc Ala	aat Asn	1109														
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 35 40 45
 Asp Leu Lys Glu Trp Asn Gln Leu Ser Ser Asp Leu Ile Ile Pro Gly
 50 55 60
 Gln Lys Leu Asn Val Ser Glu Lys Gln Thr Glu Glu Lys Lys Gln Tyr
 65 70 75 80
 Thr Ile Lys Lys Gly Asp Thr Leu Trp Lys Ile Ala Gln Lys Phe Gly
 85 90 95
 Val Ser Val Asn Asp Leu Lys Asn Trp Asn Asn Ile Lys Ser Asp Ile
 100 105 110
 Ile Tyr Pro Asn Thr Ser Ile Thr Val Asp Gly Gln Ala Thr Val Gln
 115 120 125
 Ala Ala Ala Ala Gln Pro Ala Glu Thr Lys Pro Ala Val Gln Lys Glu
 130 135 140
 Ala Lys Val Glu Lys Ala Ala Pro Ala Pro Ala Pro Lys Gln Glu Lys
 145 150 155 160
 Glu Pro Ala Ser Arg Ser Asn Val Ser Gln Ser Thr Ala Lys Glu Leu
 165 170 175
 Thr Val Thr Ala Thr Ala Tyr Thr Ala Asn Asp Gly Gly Met Thr Gly
 180 185 190
 Val Thr Ala Thr Gly Ile Asp Leu Lys Ala Asn Lys Asn Ala Lys Val
 195 200 205
 Ile Ala Val Asp Pro Asn Val Ile Pro Leu Gly Ser Lys Val Tyr Val
 210 215 220
 Glu Gly Tyr Gly Glu Ala Thr Ala Ala Asp Thr Gly Gly Ala Ile Lys
 225 230 235 240
 Gly Asn Lys Ile Asp Val Phe Val Pro Ser Lys Ser Ala Ala Lys Asn
 245 250 255

10294.000.ST25.txt
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 260 265

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 atttgccgct tcttgctgat ggaaacgagc aatgctttctt tttcaatata cttttgcacc 240
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 tagtgttatg agaaaaaaat ccgggaacgg aatcaaggac cataaaaatt ttttctggcc 360
 aaccctaaac cccggtgcgt ttaagtcgtc ataaataaga aaccagcggg ggaaaaattt 420
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 tatttaagga gagaggacca ttg aaa aag tta atc gtt tgt tta tta gct gtt 533
 Leu Lys Lys Leu Ile Val Cys Leu Leu Ala Val
 1 5 10
 tta ctg atc ttg cct gcc gga gcg tcc ctc gca gcg aaa aat caa aca 581
 Leu Leu Ile Leu Pro Ala Gly Ala Ser Leu Ala Ala Lys Asn Gln Thr
 15 20 25
 tca ggg aat tta aca aat aag caa gtc atg caa tta acc ttg cag gca 629
 Ser Gly Asn Leu Thr Asn Lys Gln Val Met Gln Leu Thr Leu Gln Ala
 30 35 40
 cgg gag cac ttt tgg aat acg atg agc ggc cac aat cca aaa gcg aaa 677
 Arg Glu His Phe Trp Asn Thr Met Ser Gly His Asn Pro Lys Ala Lys
 45 50 55
 aac tca act tgc cca tcc aaa aca ttt gaa tac cgc ggt ctt cca tat 725
 Asn Ser Thr Cys Pro Ser Lys Thr Phe Glu Tyr Arg Gly Leu Pro Tyr
 60 65 70 75
 acg tat atg tgc agt gaa ttc agc aca aaa gca aaa tta aca gac tac 773
 Thr Tyr Met Cys Ser Glu Phe Ser Thr Lys Ala Lys Leu Thr Asp Tyr
 80 85 90
 ttg acg ccg gtt ttc aca aaa gac gcc att aaa aaa ggc ttg gaa aaa 821
 Leu Thr Pro Val Phe Thr Lys Asp Ala Ile Lys Lys Gly Leu Glu Lys
 95 100 105

10294.000.ST25.txt

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ggg gac aac ctc tta gga tgg gac aag gca aaa atc aaa ctg atc tct	917
Gly Asp Asn Leu Leu Gly Trp Asp Lys Ala Lys Ile Lys Leu Ile Ser	
125 130 135	
caa aaa aac aat acc cgc act tat gaa ttt tcc gta ccg gca ttg gat	965
Gln Lys Asn Asn Thr Arg Thr Tyr Glu Phe Ser Val Pro Ala Leu Asp	
140 145 150 155	
gga tcg gtg act gcg aaa aga aag atc acg ttt gtg aaa gaa aac aac	1013
Gly Ser Val Thr Ala Lys Arg Lys Ile Thr Phe Val Lys Glu Asn Asn	
160 165 170	
aaa tgg aaa atc aat cag ctc gat gct gcc atc taaacgaaaa agctaattgtc	1066
Lys Trp Lys Ile Asn Gln Leu Asp Ala Ala Ile	
175 180	
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35 40 45	
Asn Thr Met Ser Gly His Asn Pro Lys Ala Lys Asn Ser Thr Cys Pro	
50 55 60	

Ser Lys Thr Phe Glu Tyr Arg Gly Leu Pro Tyr Thr Tyr Met Cys Ser
65 70 75 80

Glu Phe Ser Thr Lys Ala Lys Leu Thr Asp Tyr Leu Thr Pro Val Phe
85 90 95

Thr Lys Asp Ala Ile Lys Lys Gly Leu Glu Lys Tyr Asn Ile Ile Ser
100 105 110

Tyr Lys Gly Lys Met Ala Val Pro Val Gly Asp Gly Asp Asn Leu Leu
115 120 125

Gly Trp Asp Lys Ala Lys Ile Lys Leu Ile Ser Gln Lys Asn Asn Thr
130 135 140

Arg Thr Tyr Glu Phe Ser Val Pro Ala Leu Asp Gly Ser Val Thr Ala
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Lys Arg Lys Ile Thr Phe Val Lys Glu Asn Asn Lys Trp Lys Ile Asn
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<213> Bacillus licheniformis

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Lys Trp Glu Glu Lys Ala Val Glu Glu Ala Lys Lys Arg Tyr Pro Glu
 35 40 45

Ala Glu Val Arg Leu Thr Lys Lys Val Trp Asp Arg Lys Arg Ala Asp
 50 55 60

Glu Ala Val Lys Gln Tyr His Val Thr Leu Ser Glu Gly Asn Lys Asn
 65 70 75 80

Phe Gly Val Phe Val Thr Ile Ser Phe Glu Pro Ala Thr His Lys Ile
 85 90 95

Asn Lys Val Val Val Glu Glu Tyr Lys
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 ctagtttgac atcttctaaa agaaggagcg gattttg atg ggt aaa cag caa atg 535
 Met Gly Lys Gln Gln Met
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aaa aaa acg atg tcg cag acg gat gtg cta ttt tta gcg atc gga gct 583
 Lys Lys Thr Met Ser Gln Thr Asp Val Leu Phe Leu Ala Ile Gly Ala
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atg ctc ggc tgg ggc tgg gtc gtc ctt tcc ggc gac tgg att tcg aca 631
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 25 30 35

10294.000.ST25.txt

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gtc Val 55	atc Ile	tta Leu	atc Ile	ggg Gly 60	tta Leu 60	acg Thr	tac Tyr	gcg Ala	gag Glu 65	ctg Leu 65	tct Ser	tct Ser	gcc Ala	atc Ile	cct Pro 70	727
gaa Glu	acg Thr	ggt Gly	ggc Gly	ggc Gly 75	ttg Leu	att Ile	ttc Phe	gtc Val	tac Tyr 80	agg Arg	gcg Ala	ttc Phe	gga Gly 85	cga Arg 85	aaa Lys	775
acg Thr	gct Ala	ttt Phe 90	gtc Val 90	gcc Ala	gct Ala	tgg Trp	ggt Gly	gtg Val 95	ctg Leu	ttc Phe	ggc Gly	tat Tyr	gtt Val 100	tcg Ser	gtg Val	823
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ctc Leu	ggg Gly 280	aac Asn	cag Gln	ctg Leu	ttc Phe	ggc Gly 285	acg Thr	gtg Val	ctt Leu	gtc Val	ctc Leu 290	ggc Gly	ggc Gly	gtc Val	gcc Ala	1399
gga Gly 295	atc Ile	att Ile	acg Thr	agc Ser	tgg Trp 300	aac Asn	gca Ala	ttt Phe	atc Ile	atc Ile 305	ggc Gly	gcg Ala	agc Ser	cgg Arg	att Ile 310	1447

10294.000.ST25.txt

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gcg ctg gcg ttt ttt gcc ccg ctg ctc gga cgc cct gcc ctt gtt tgg Ala Leu Ala Phe Phe Ala Pro Leu Leu Gly Arg Pro Ala Leu Val Trp 345 350 355	1591
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ctc aca tgg ccg tat gag tgg ctg atc ttg gcg gga tgg aca ttg atc Leu Thr Trp Pro Tyr Glu Trp Leu Ile Leu Ala Gly Trp Thr Leu Ile 425 430 435	1831
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<212> PRT

<213> Bacillus licheniformis

<400> 186

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 35 40 45
 Ile Ile Gly Gly Ile Leu Val Ile Leu Ile Gly Leu Thr Tyr Ala Glu
 50 55 60
 Leu Ser Ser Ala Ile Pro Glu Thr Gly Gly Gly Leu Ile Phe Val Tyr
 65 70 75 80
 Arg Ala Phe Gly Arg Lys Thr Ala Phe Val Ala Ala Trp Gly Val Leu
 85 90 95
 Phe Gly Tyr Val Ser Val Ile Thr Phe Glu Ala Val Ala Leu Pro Thr
 100 105 110
 Val Ile Asp Tyr Val Leu Pro Val Glu His Gln Gly Phe Leu Trp Ser
 115 120 125
 Leu Ser Gly Trp Asp Val Tyr Val Thr Trp Val Leu Ile Gly Ser Gly
 130 135 140
 Gly Ala Val Val Leu Thr Ala Leu Asn Tyr Phe Gly Val Lys Pro Ala
 145 150 155 160
 Ala Ile Phe Gln Ser Val Phe Thr Ile Ala Ile Ile Ala Thr Gly Phe
 165 170 175
 Leu Leu Leu Gly Gly Ala Leu Val Asn Gly Asp Phe Glu His Val Gln
 180 185 190
 Pro Leu Phe Lys Asp Gly Phe Ser Gly Met Met Ser Val Leu Val Met
 195 200 205
 Ile Pro Phe Leu Phe Val Gly Phe Asp Val Ile Pro Gln Val Ala Ala
 210 215 220
 Glu Ile Asn Ala Pro Lys Lys Ile Ile Gly Lys Ile Leu Ile Ile Ser
 225 230 235 240
 Ile Ile Ser Ala Val Val Phe Tyr Leu Leu Ile Val Phe Gly Val Thr
 245 250 255
 Met Gly Leu Ser Glu Ser Glu Leu Ala Thr Thr Ser Leu Ala Thr Ala
 260 265 270

Asp Ala Met Val Asn Leu Leu Gly Asn Gln Leu Phe Gly Thr Val Leu
 275 280 285
 Val Leu Gly Gly Val Ala Gly Ile Ile Thr Ser Trp Asn Ala Phe Ile
 290 295 300
 Ile Gly Ala Ser Arg Ile Leu Phe Ala Met Ser Glu Lys Gly Met Val
 305 310 315 320
 Pro Lys Trp Phe Gly Phe Ile His Pro Lys Tyr Lys Thr Pro Thr Asn
 325 330 335
 Ala Ile Leu Phe Leu Gly Ala Leu Ala Phe Phe Ala Pro Leu Leu Gly
 340 345 350
 Arg Pro Ala Leu Val Trp Ile Val Asn Ala Gly Gly Thr Gly Ile Ile
 355 360 365
 Val Gly Tyr Leu Ile Val Ser Ile Ala Phe Met Lys Leu Arg Lys Thr
 370 375 380
 Glu Pro Asp Leu His Arg Pro Tyr Lys Ile Asn Lys Trp Lys Thr Thr
 385 390 395 400
 Gly Ile Ser Ala Ile Leu Leu Ser Val Ile Phe Leu Ala Phe Tyr Leu
 405 410 415
 Pro Gly Met Pro Ala Ala Leu Thr Trp Pro Tyr Glu Trp Leu Ile Leu
 420 425 430
 Ala Gly Trp Thr Leu Ile Gly Phe Leu Leu Tyr Asn Ser Ser Ser Lys
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cagcgatttat ttccgtgacg acgactcaat taagatcgat gctgggaggc atgaatatga      240
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catttttggga gggtattttt ttg aag gtc ttt ctt aaa gct gta cct atg ttg      533
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Trp Leu Arg Phe Phe Leu Phe Val Pro Asn Val Phe Ala Ala Asn Ser
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gtc aca aga ttg gac ggt gca aac cga tat gag gtt gcg gtg aac gtt      629
Val Thr Arg Leu Asp Gly Ala Asn Arg Tyr Glu Val Ala Val Asn Val
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tcc aag cag ggg tgg aca agt gca agc act gtg att gtt gca aat gga      677
Ser Lys Gln Gly Trp Thr Ser Ala Ser Thr Val Ile Val Ala Asn Gly
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aag gca tat gca gac gtc ctt tca gcg act cca ttt gcc tat cga aac      725
Lys Ala Tyr Ala Asp Val Leu Ser Ala Thr Pro Phe Ala Tyr Arg Asn
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Asn Ala Pro Val Leu Leu Thr Glu Ala Ser Lys Leu Pro Thr Ala Thr
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Val	Val	Gly	Gly	Glu	Val	Ser	Ile	Ser	Ser	Ser	Val	Tyr	Lys	Gln	Leu	
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Lys	Gln	Asn	Arg	Pro	Met	Met	Phe	Thr	Asn	Ala	Ser	Ser	Leu	Pro	Thr	
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Gln	Asn	Arg	Leu	Tyr	Val	Ala	Leu	Asn	Thr	Lys	Asn	Arg	Gly	Val	Lys	
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Ile	Gly	Asn	Phe	His	Val	Ile	Arg	Glu	Ser	Lys	Met	Pro	Ser	Cys	Leu	
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 480 485 490

gtt gct tac tat taaaatataa acagaaaact cgtttttcga aaaattgcct 2025
 Val Ala Tyr Tyr
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<212> PRT

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Gly Ala Asn Arg Tyr Glu Val Ala Val Asn Val Ser Lys Gln Gly Trp
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Thr Ser Ala Ser Thr Val Ile Val Ala Asn Gly Lys Ala Tyr Ala Asp
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Val Leu Ser Ala Thr Pro Phe Ala Tyr Arg Asn Asn Ala Pro Val Leu
 65 70 75 80

Leu Thr Glu Ala Ser Lys Leu Pro Thr Ala Thr Lys Asn Arg Ile Ser
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Gln Leu Lys Pro Ser Lys Val Ile Val Ile Gly Gly Thr Val Ser Val
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 Val Ser Ile Ser Ser Ser Val Tyr Lys Gln Leu Ala Ser Pro Thr Arg
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 Ile Gly Gly Ser Asn Arg Tyr Glu Val Ala Ala Asn Val Val Lys Lys
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 Ala Asp Gly Leu Thr Gly Ser Val Leu Ala Ala Lys Gln Asn Arg Pro
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 Lys Lys Ile Phe Ile Asp Ala Gly His Gly Gly Thr Asp Ser Gly Ala
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Gln Ser Asn His Ala Asp Leu Phe Val Ser Ile His Ala Asn Ser Ala
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Val Ala Leu Asn Thr Lys Asn Arg Gly Val Lys Ile Gly Asn Phe His
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Val Ile Arg Glu Ser Lys Met Pro Ser Cys Leu Val Glu Leu Ala Phe
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<222> (501)..(1667)

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taaaagaagg agtaccgcgac atg gca aga aca tac aga acg cga ata aag aaa 533
 Met Ala Arg Thr Tyr Arg Thr Arg Ile Lys Lys
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 Arg Lys Lys Gln Lys Thr Lys Arg Arg Leu Ile Ile Phe Ser Phe Leu
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 Val Val Cys Gly Leu Ile Tyr Leu Ala Leu Pro Ser Gly Met Arg Asp
 30 35 40

cac cag gaa aac caa ttg caa gca act gaa aaa aag gca cag cct gaa 677
 His Gln Glu Asn Gln Leu Gln Ala Thr Glu Lys Lys Ala Gln Pro Glu
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gat acc gtc ttt tat gtg ggg tca tca caa aaa gcg att att gca acg Asp Thr Val Phe Tyr Val Gly Ser Ser Gln Lys Ala Ile Ile Ala Thr 125 130 135	917
gca att tta cag ctg gag gaa aaa gga ttg cta tct gta aat gac cct Ala Ile Leu Gln Leu Glu Glu Lys Gly Leu Leu Ser Val Asn Asp Pro 140 145 150 155	965
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cgc gga tat att tcg ccg gaa gat tta att aaa gat atc gaa aaa cgg Arg Gly Tyr Ile Ser Pro Glu Asp Leu Ile Lys Asp Ile Glu Lys Arg 190 195 200	1109
ggt gta aaa tac cca aca ggg aaa tgg gat tat aga gac tcc aat tac Gly Val Lys Tyr Pro Thr Gly Lys Trp Asp Tyr Arg Asp Ser Asn Tyr 205 210 215	1157
tcg gtt ctg gca tac att gtt tcc atg gta agc ggt gaa cca gtc gac Ser Val Leu Ala Tyr Ile Val Ser Met Val Ser Gly Glu Pro Val Asp 220 225 230 235	1205
caa tac atc aaa aag cat att ttt aaa cct gcc ggt atg aaa cat gca Gln Tyr Ile Lys Lys His Ile Phe Lys Pro Ala Gly Met Lys His Ala 240 245 250	1253
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tca cag ctt tac ggg gcc ggt gat att tat atg acc gct tat gac atg Ser Gln Leu Tyr Gly Ala Gly Asp Ile Tyr Met Thr Ala Tyr Asp Met 285 290 295	1397
tat ttg ttt gat aaa gca ctt tac gaa aga aaa atc att tcc aat gaa Tyr Leu Phe Asp Lys Ala Leu Tyr Glu Arg Lys Ile Ile Ser Asn Glu 300 305 310 315	1445
agt ttt atg aaa atg ttt acg ccg aat aaa gca aca tac ggc atg ggc Ser Phe Met Lys Met Phe Thr Pro Asn Lys Ala Thr Tyr Gly Met Gly 320 325 330	1493

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Phe Tyr Val Ser Pro Gly Ser Tyr Ser Ser His Gly Val Met Pro Gly
335 340 345

tac aac ata tta aac agt ttc agt ctg aca ggg agc aga tac gtc att 1589
Tyr Asn Ile Leu Asn Ser Phe Ser Leu Thr Gly Ser Arg Tyr Val Ile
350 355 360

cta ttt tca aac atc caa aac aac att aag tct ttt ggc agt gtg aat 1637
Leu Phe Ser Asn Ile Gln Asn Asn Ile Lys Ser Phe Gly Ser Val Asn
365 370 375

aat cgg atc ttc tct att tta aat gga ttt tgaacagcag agaaagtttt 1687
Asn Arg Ile Phe Ser Ile Leu Asn Gly Phe
380 385

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<212> PRT

<213> Bacillus licheniformis

<400> 192

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Ile Tyr Leu Ala Leu Pro Ser Gly Met Arg Asp His Gln Glu Asn Gln
35 40 45

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Leu Gln Ala Thr Glu Lys Lys Ala Gln Pro Glu Ala Lys Lys Lys Pro
50 55 60

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Thr Gln Asn Glu Thr Lys Lys Ser Lys Ile Val Thr Lys Asn Asp Asn
65 70 75 80

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Ala Gln Leu Asp Gln Tyr Leu Lys Ser Ile Gly Phe Ser Gly Thr Ala
85 90

Leu Ile Val Glu Asp Gly Lys Val Val Thr Ser Lys Gly Tyr Leu Tyr
100 105 110

Ala Asn Arg Glu Glu Met Val Pro Asn Thr Pro Asp Thr Val Phe Tyr
115 120 125

Val Gly Ser Ser Gln Lys Ala Ile Ile Ala Thr Ala Ile Leu Gln Leu
130 135 140

Glu Glu Lys Gly Leu Leu Ser Val Asn Asp Pro Val Ser Lys Tyr Leu
145 150 155 160

Pro Asn Phe Pro Asn Gly Ser Lys Ile Thr Leu Tyr His Phe Leu Thr
165 170 175

His Thr Ser Gly Ile Arg Gly His Lys Glu Gly Arg Gly Tyr Ile Ser
180 185 190

Pro Glu Asp Leu Ile Lys Asp Ile Glu Lys Arg Gly Val Lys Tyr Pro
195 200 205

Thr Gly Lys Trp Asp Tyr Arg Asp Ser Asn Tyr Ser Val Leu Ala Tyr
210 215 220

Ile Val Ser Met Val Ser Gly Glu Pro Val Asp Gln Tyr Ile Lys Lys
225 230 235 240

His Ile Phe Lys Pro Ala Gly Met Lys His Ala Gly Phe Tyr Lys Thr
245 250 255

Phe Ala Lys Glu Ser Asn Pro Ser Thr Gly Tyr Lys Leu Asn Leu Gln
260 265 270

Lys Lys Leu Tyr Thr Pro Asp Met Pro Asp Leu Ser Gln Leu Tyr Gly
275 280 285

Ala Gly Asp Ile Tyr Met Thr Ala Tyr Asp Met Tyr Leu Phe Asp Lys
290 295 300

Ala Leu Tyr Glu Arg Lys Ile Ile Ser Asn Glu Ser Phe Met Lys Met
305 310 315 320

Phe Thr Pro Asn Lys Ala Thr Tyr Gly Met Gly Phe Tyr Val Ser Pro
325 330 335

Gly Ser Tyr Ser Ser His Gly Val Met Pro Gly Tyr Asn Ile Leu Asn
340 345 350

Ser Phe Ser Leu Thr Gly Ser Arg Tyr Val Ile Leu Phe Ser Asn Ile
 355 360 365

Gln Asn Asn Ile Lys Ser Phe Gly Ser Val Asn Asn Arg Ile Phe Ser
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Ile Leu Asn Gly Phe
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<212> DNA

<213> Bacillus licheniformis

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<222> (501)..(989)

<223>

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 gctcaatgct gcgatgatca gcgttttaac gggccagccg cttcgtttca attgaccgcg 180
 gaaagccgcg aacaagagca gggatgatgcc gccgacagcc attctgacag cgccgaacac 240
 aagaggtgcc gcctcttttcg gcgcaaatgc ctgggttgtt cccgtcgttc cccataaaat 300
 tgccgcaagc aagacaaaca gaaccgatac tttcatacta acgatctctc cctactcgat 360
 cattcagaac tttttctatt gtaagataag tttgcggatt tttgaatcgc cgcttcggaa 420
 atttccctga aaagaggaaa tattcaacgc tggccgaatt catataatgg ccaaaaaaca 480
 attaaagtcg gaggaagcgg atg aaa aaa cga aca gtt tta ttc ttc ttg ttg 533
 Met Lys Lys Arg Thr Val Leu Phe Phe Leu Leu
 1 5 10
 atc tgg ctc gcc gga tgt gcg agc gcc caa gag gct gag gaa caa acc 581
 Ile Trp Leu Ala Gly Cys Ala Ser Ala Gln Glu Ala Glu Glu Gln Thr
 15 20 25
 aaa tgg gtg aac agc gaa cag aaa gcg att gag aac ggc att cgt tat 629
 Lys Trp Val Asn Ser Glu Gln Lys Ala Ile Glu Asn Gly Ile Arg Tyr
 30 35 40
 gaa agc att aca aaa gac gat att ata gac aaa atc gat tta aac ggt 677
 Glu Ser Ile Thr Lys Asp Asp Ile Ile Asp Lys Ile Asp Leu Asn Gly
 45 50 55
 gaa caa gtc gtc gtt ttt cga ttc ggc gat tcg gag gga gag ggg att 725
 Glu Gln Val Val Val Phe Arg Phe Gly Asp Ser Glu Gly Glu Gly Ile
 60 65 70 75

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Gly Leu Ala His Ile Lys Arg Glu Asn Gly Asn Tyr Gln Trp Tyr Arg
80 85 90

gac tta aat tac gca att gta aaa tcg gac cac ccg aaa acg gag aat 821
Asp Leu Asn Tyr Ala Ile Val Lys Ser Asp His Pro Lys Thr Glu Asn
95 100 105

gcg gaa gct tcc gcg ccg ttc aca acc cct aag gga aga aag tac acg 869
Ala Glu Ala Ser Ala Pro Phe Thr Thr Pro Lys Gly Arg Lys Tyr Thr
110 115 120

tta tat aca ggg gat gca gat cgc ctg aat ggt aca ttt gag act gat 917
Leu Tyr Thr Gly Asp Ala Asp Arg Leu Asn Gly Thr Phe Glu Thr Asp
125 130 135

gac ggg ctt cat ttg gag ccg gtg gtc gat caa aaa acg ggc atg tat 965
Asp Gly Leu His Leu Glu Pro Val Val Asp Gln Lys Thr Gly Met Tyr
140 145 150 155

tat cag atc gtg cag gat tcg gac tgaaatgaaa caaaaatgct gtcgggttgt 1019
Tyr Gln Ile Val Gln Asp Ser Asp
160

tcccgacagc atttcatttt ttacgatttc tttttccgca ctgtcaagag cagcgcagca 1079

cctccaagaa gcacggcgag gatcgacagg atcaggggaag cggtttgaat cccttgcct 1139

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ccaggctgaa tgccgccgtt ttcggcttcc cacgtcaccc ttgttacttt ttcgtttttg 1439

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<211> 163

<212> PRT

<213> Bacillus licheniformis

<400> 194

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Glu Gln Lys Ala Ile Glu Asn Gly Ile Arg Tyr Glu Ser Ile Thr Lys
35 40 45

Asp Asp Ile Ile Asp Lys Ile Asp Leu Asn Gly Glu Gln Val Val Val
50 55 60

10294.000.ST25.txt

Phe Arg Phe Gly Asp Ser Glu Gly Glu Gly Ile Gly Leu Ala His Ile
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Lys Arg Glu Asn Gly Asn Tyr Gln Trp Tyr Arg Asp Leu Asn Tyr Ala
85 90 95

Ile Val Lys Ser Asp His Pro Lys Thr Glu Asn Ala Glu Ala Ser Ala
100 105 110

Pro Phe Thr Thr Pro Lys Gly Arg Lys Tyr Thr Leu Tyr Thr Gly Asp
115 120 125

Ala Asp Arg Leu Asn Gly Thr Phe Glu Thr Asp Asp Gly Leu His Leu
130 135 140

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<212> DNA

<213> Bacillus licheniformis

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<222> (501)..(1490)

<223>

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aagaatctag ttgagcgggt gagcagggga ttccttatta tgactgcat tttgcacatt 180
tctccatttt cctgcaaggt caaaagacat agttcttaag ttttggattt ttggtgtgtt 240
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aacagggttt ttcgaacaga atgtcaaata gattagatat ttcataagaa caagggggaa 360
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gttcttagaa aaaaatgcgg ctaaatatat atttatagat tgtaaacgct gtcttgcct 480
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10294.000.ST25.txt
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Leu	Cys	Leu	Phe	Phe	Leu	Tyr	Val	Tyr	Asp	Tyr	Ser	Arg	Gly	Asp	Lys	
			15					20					25			
gcc	ggt	tct	gca	gaa	gaa	agc	agg	agg	cct	gcg	gcc	gca	ggc	agt	ctg	629
Ala	Gly	Ser	Ala	Glu	Glu	Ser	Arg	Arg	Pro	Ala	Ala	Ala	Gly	Ser	Leu	
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tcc	gaa	aaa	tac	gtg	atg	gtc	acg	ttt	caa	tcg	gga	atc	gaa	tat	tgg	677
Ser	Glu	Lys	Tyr	Val	Met	Val	Thr	Phe	Gln	Ser	Gly	Ile	Glu	Tyr	Trp	
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aag	agc	ggt	ctg	aaa	ggc	ttt	gag	gat	gcc	gcg	cag	ctt	ttc	aac	gtc	725
Lys	Ser	Gly	Leu	Lys	Gly	Phe	Glu	Asp	Ala	Ala	Gln	Leu	Phe	Asn	Val	
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tct	gtc	gag	tat	cgg	ggg	gcg	gcc	cat	tat	gat	gtc	cat	gag	caa	acg	773
Ser	Val	Glu	Tyr	Arg	Gly	Ala	Ala	His	Tyr	Asp	Val	His	Glu	Gln	Thr	
				80					85					90		
acc	gtc	ctc	gag	cag	gtg	att	gca	aaa	aaa	ccg	gcg	gga	atc	gct	gtt	821
Thr	Val	Leu	Glu	Gln	Val	Ile	Ala	Lys	Lys	Pro	Ala	Gly	Ile	Ala	Val	
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tcg	gca	ata	aac	cca	aaa	gct	tta	aac	cct	gtc	atc	gac	aag	gcg	cac	869
Ser	Ala	Ile	Asn	Pro	Lys	Ala	Leu	Asn	Pro	Val	Ile	Asp	Lys	Ala	His	
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Glu	Gln	Gly	Ile	Pro	Ile	Val	Leu	Phe	Asp	Ser	Asp	Ala	Pro	Leu	Ser	
	125					130					135					
aaa	gct	tct	aca	tat	atc	ggc	aca	aat	aat	atg	gaa	gcg	ggt	gct	gtg	965
Lys	Ala	Ser	Thr	Tyr	Ile	Gly	Thr	Asn	Asn	Met	Glu	Ala	Gly	Ala	Val	
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gcc	gca	agg	cga	atg	gcc	gaa	ttt	ttg	aat	gga	aag	gga	gaa	acc	gcg	1013
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				160					165					170		
gtc	att	acc	cag	ccg	cag	cag	tac	aat	cat	cag	gaa	agg	acg	aag	ggc	1061
Val	Ile	Thr	Gln	Pro	Gln	Gln	Tyr	Asn	His	Gln	Glu	Arg	Thr	Lys	Gly	
			175					180					185			
ttt	gaa	caa	acg	atc	aag	caa	aaa	tac	ccg	aac	atg	aag	gtt	gcc	gcg	1109
Phe	Glu	Gln	Thr	Ile	Lys	Gln	Lys	Tyr	Pro	Asn	Met	Lys	Val	Ala	Ala	
		190					195					200				
gtt	ttg	gac	gga	aaa	ggg	gat	gag	ctg	acg	tcg	aaa	aaa	gaa	gcg	gcg	1157
Val	Leu	Asp	Gly	Lys	Gly	Asp	Glu	Leu	Thr	Ser	Lys	Lys	Glu	Ala	Ala	
	205					210					215					
aag	att	ttg	gag	gaa	aat	ccg	tcc	atc	aaa	gga	att	ttc	acg	act	gaa	1205
Lys	Ile	Leu	Glu	Glu	Asn	Pro	Ser	Ile	Lys	Gly	Ile	Phe	Thr	Thr	Glu	
	220				225					230					235	
gcc	aat	gga	gcg	agc	ggc	gtg	gcc	cgt	gct	gtg	aag	gag	gcg	gga	ctt	1253
Ala	Asn	Gly	Ala	Ser	Gly	Val	Ala	Arg	Ala	Val	Lys	Glu	Ala	Gly	Leu	
				240					245					250		
gaa	ggg	gaa	gta	tgt	atc	atc	ggc	ttt	gat	aaa	gac	aag	aaa	acg	ctg	1301
Glu	Gly	Glu	Val	Cys	Ile	Ile	Gly	Phe	Asp	Lys	Asp	Lys	Lys	Thr	Leu	
			255					260					265			
gac	ggc	atc	aaa	aac	gga	tcg	att	tcc	gcg	aca	atg	agc	cag	gac	aca	1349

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 Trp Gln Met Gly Tyr Trp Ser Leu His Met Leu Phe Phe Ser Asn His
 285 290 295

cat ctg aag cat gaa cgc ccg ctt ccg gcc gca atc gac aca ggc att 1445
 His Leu Lys His Glu Arg Pro Leu Pro Ala Ala Ile Asp Thr Gly Ile
 300 305 310 315

acc atc ata acg aaa gaa aat gtg gca gcc tat tat gcg aat gat 1490
 Thr Ile Ile Thr Lys Glu Asn Val Ala Ala Tyr Tyr Ala Asn Asp
 320 325 330

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 tgaaaaacag gtgatcgacc aaacactgca gctgatcggc gaagtgaaca agacggctga 1670
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 tgagatgatc agcaatgaga tgtatgaacg cacgccgaca gatttgacaa aagaaccatg 1910
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<211> 330

<212> PRT

<213> Bacillus licheniformis

<400> 196

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 20 25 30

Glu Ser Arg Arg Pro Ala Ala Ala Gly Ser Leu Ser Glu Lys Tyr Val
 35 40 45

Met Val Thr Phe Gln Ser Gly Ile Glu Tyr Trp Lys Ser Gly Leu Lys
 50 55 60

Gly Phe Glu Asp Ala Ala Gln Leu Phe Asn Val Ser Val Glu Tyr Arg
 65 70 75 80

Gly Ala Ala His Tyr Asp Val His Glu Gln Thr Thr Val Leu Glu Gln
 85 90 95

Val Ile Ala Lys Lys Pro Ala Gly Ile Ala Val Ser Ala Ile Asn Pro
 100 105 110
 Lys Ala Leu Asn Pro Val Ile Asp Lys Ala His Glu Gln Gly Ile Pro
 115 120 125
 Ile Val Leu Phe Asp Ser Asp Ala Pro Leu Ser Lys Ala Ser Thr Tyr
 130 135 140
 Ile Gly Thr Asn Asn Met Glu Ala Gly Ala Val Ala Ala Arg Arg Met
 145 150 155 160
 Ala Glu Phe Leu Asn Gly Lys Gly Glu Thr Ala Val Ile Thr Gln Pro
 165 170 175
 Gln Gln Tyr Asn His Gln Glu Arg Thr Lys Gly Phe Glu Gln Thr Ile
 180 185 190
 Lys Gln Lys Tyr Pro Asn Met Lys Val Ala Ala Val Leu Asp Gly Lys
 195 200 205
 Gly Asp Glu Leu Thr Ser Lys Lys Glu Ala Ala Lys Ile Leu Glu Glu
 210 215 220
 Asn Pro Ser Ile Lys Gly Ile Phe Thr Thr Glu Ala Asn Gly Ala Ser
 225 230 235 240
 Gly Val Ala Arg Ala Val Lys Glu Ala Gly Leu Glu Gly Glu Val Cys
 245 250 255
 Ile Ile Gly Phe Asp Lys Asp Lys Lys Thr Leu Asp Gly Ile Lys Asn
 260 265 270
 Gly Ser Ile Ser Ala Thr Met Ser Gln Asp Thr Trp Gln Met Gly Tyr
 275 280 285
 Trp Ser Leu His Met Leu Phe Phe Ser Asn His His Leu Lys His Glu
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 305 310 315 320
 Glu Asn Val Ala Ala Tyr Tyr Ala Asn Asp
 325 330

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<211> 1677

<212> DNA

<223>

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 Glu Lys Asn Asn Leu Tyr Leu Arg Pro Pro Arg Gly Ile Phe Ser Glu
 160 165 170
 cgg gtg ctc gaa gaa acg aaa aag ctc ggc tat caa acg gta ttc tgg 1061
 Arg Val Leu Glu Glu Thr Lys Lys Leu Gly Tyr Gln Thr Val Phe Trp
 175 180 185
 tct gtt gct ttt gtc gat tgg aaa atc aat gcc caa aaa ggg tgg cgc 1109
 Ser Val Ala Phe Val Asp Trp Lys Ile Asn Ala Gln Lys Gly Trp Arg
 190 195 200
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 Tyr Ala Tyr Asp Asn Met Met Lys Gln Ala His Pro Gly Ala Ile Tyr
 205 210 215
 ctg ctt cac acc gtc ttc agg cga tca ccg act tgaaaaaaga aggttataca 1210
 Leu Leu His Thr Val Phe Arg Arg Ser Pro Thr
 220 225 230
 tttaaaagcc tcgatgacct gatgtttgaa aaatctatga tgcttgagac ccttgaaaga 1270
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 <213> *Bacillus licheniformis*

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 35 40 45
 Thr Asn Leu Leu Gln Gln Tyr Asp Ala Phe Tyr Leu Gly Asn Thr Lys
 50 55 60

10294.000.ST25.txt

Glu Lys Thr Ile Tyr Leu Thr Phe Asp Asn Gly Tyr Glu Asn Gly Tyr
65 70 75 80

Thr Pro Gln Val Leu Asp Val Leu Lys Lys Gln Asn Val Lys Ala Ala
85 90 95

Phe Phe Val Thr Gly His Phe Val Lys Asp Gln Pro Glu Leu Ile Lys
100 105 110

Arg Met Ala Glu Glu Gly His Ile Ile Gly Asn His Ser Tyr His His
115 120 125

Pro Asp Leu Thr Thr Lys Thr Ser Arg Val Ile Gln Glu Glu Leu Glu
130 135 140

Ser Val Asp Glu Glu Val Tyr Lys Ile Thr Gly Glu Lys Asn Asn Leu
145 150 155 160

Tyr Leu Arg Pro Pro Arg Gly Ile Phe Ser Glu Arg Val Leu Glu Glu
165 170 175

Thr Lys Lys Leu Gly Tyr Gln Thr Val Phe Trp Ser Val Ala Phe Val
180 185 190

Asp Trp Lys Ile Asn Ala Gln Lys Gly Trp Arg Tyr Ala Tyr Asp Asn
195 200 205

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Phe Arg Arg Ser Pro Thr
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